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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>G01N 33/574, 33/577, C07K 16/30, A61K 39/395, 47/48, C12Q 1/68, G01N 33/543</b>		A2	(11) International Publication Number: <b>WO 98/37418</b> (43) International Publication Date: <b>27 August 1998 (27.08.98)</b>
(21) International Application Number: <b>PCT/US98/03690</b>		(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: <b>25 February 1998 (25.02.98)</b>		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(30) Priority Data: 08/806,596 25 February 1997 (25.02.97) US 08/904,809 1 August 1997 (01.08.97) US Not furnished 9 February 1998 (09.02.98) US			
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(54) Title: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for diagnosing prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. The inventive polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. Nucleic acid sequences for preparing probes, primers, and polypeptides are also provided.

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## COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS FOR THEIR USE

### TECHNICAL FIELD

The present invention relates generally to the treatment and monitoring of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein. Such polypeptides may be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of prostate cancer, and possibly other tumor types, in a patient.

### BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into diagnosis and therapy of the disease, prostate cancer remains difficult to detect and to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited diagnostic and therapeutic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved and diagnostic methods for prostate cancer.

## SUMMARY OF THE INVENTION

The present invention provides methods for immunodiagnosis of prostate cancer, together with kits for use in such methods. Polypeptides are disclosed which comprise at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224 and variants thereof. Such polypeptides may be usefully employed in the diagnosis and monitoring of prostate cancer.

In one specific aspect of the present invention, methods are provided for detecting prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample a protein or polypeptide that binds to the binding agent. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody.

In related aspects, methods are provided for monitoring the progression of prostate cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent; (c) repeating steps (a) and (b); and comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of prostate cancer.

The present invention further provides methods for detecting prostate cancer comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with a first and a second oligonucleotide primer in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers. In a preferred embodiment, at least one of the

oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In a further aspect, the present invention provides a method for detecting prostate cancer in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a DNA molecule that encodes one of the above polypeptides; and (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe. Preferably, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a partial sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177 and 179-224.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunodiagnosis and monitoring of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant thereof such a protein, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-11, 115-171, 173-175, 177, 179-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide"

encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to

generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames

of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides and/or fusion proteins of the present invention may be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide and/or fusion protein prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides and/or fusion proteins capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of

one or more of the above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about  $10^3$  L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphteria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID Nos: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al. *Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may also be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NO: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid

expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from

about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLES

#### EXAMPLE 1

##### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size

being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara et al. (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and Sful, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H<sub>2</sub>O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library(prostate subtraction 1.

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID No: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID Nos: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID Nos: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID Nos: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID Nos:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID Nos: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID Nos: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID Nos: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ

ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues

examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to

be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

### Example 3

#### ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79, and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant

homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

#### EXAMPLE 4 SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun  
Dillon, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER  
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 23-FEB-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.  
(B) REGISTRATION NUMBER: 31,392  
(C) REFERENCE/DOCKET NUMBER: 210121.428C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900  
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TTTTTCACAG TATAACAGCT CTTTATTCT GTGAGTTCTA CTAGGAAATC

ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATAACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGTC	CAGTCCCTCT	CCTTAACCTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCCTCC	180
CTCCTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCGCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCCTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTTGTG	CCCTTAGTG	AGGGTTAATT	420
GCGCGCTTGG	CGTAATCATG	GTCATAACTG	TTTCCTGTGT	GAAATTGTTA	TCCGCTCAC	480
ATTCACACACA	ACATACGAGC	CGGAAGCATA	AAGTGTAAAG	CCTGGGTGC	CTAATGAGTG	540
ANCTAACTCA	CATTAATTGC	GTTGCGCTCA	CTGNCCGCTT	TCCAGTCNGG	AAAACGTGCG	600
TGCCAGCTGC	ATTAATGAAT	CGGCCAACGC	NCGGGGAAAA	GCGGTTGCG	TTTGGGGGC	660
TCTCCGCTT	CTCGCTCACT	NANTCCTGCG	CTCGGTCTNT	CGGCTGCGGG	GAACGGTATC	720
ACTCCTCAAA	GGNGGTATTA	CGGTTATCCN	NAAATCNGGG	GATACCCNGG	AAAAAANTTT	780
AAACAAAGGG	CANCAAAGGG	CNGAAACGTA	AAAA			814

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT	TGGATGGTGG	AGCACCTTTC	TATAACGACTT	ACAGGACAGC	AGATGGGGAA	60
TTCATGGCTG	TTGGAGCAAT	AGAACCCCCAG	TTCTACGAGC	TGCTGATCAA	AGGACTTGGG	120
CTAAAGTCTG	ATGAACCTTCC	CAATCAGATG	AGCATGGATG	ATTGGCCAGA	AATGAAGAAG	180
AAGTTGCAG	ATGTATTTGC	AAAGAACAGC	AAGGCAGAGT	GGTGTCAAAT	CTTGACGGC	240
ACAGATGCCT	GTGTGACTCC	GGTTCTGACT	TTTGAGGAGG	TTGTTCATCA	TGATCACAAC	300
AAGGAACGGG	GCTCGTTAT	CACCACTGAG	GAGCAGGACG	TGAGCCCCCG	CCCTGCACCT	360
CTGCTGTTAA	ACACCCCGC	CATCCCTTCT	TCAAAAGGG	ATCCACTAGT	TCTAGAAGCG	420
GCCGCCACCG	CGGTGGAGCT	CCAGCTTTG	TTCCCTTTAG	TGAGGGTTAA	TTGCGCGCTT	480
GGCGTAATCA	TGGTCATAGC	TGTTTCTGT	GTGAAATTGT	TATCCGCTCA	CAATTCCCCC	540
AACATACGAG	CCGGAACATA	AAGTGTAAAG	CCTGGGTGC	CTAATGANTG	AGCTAACTCN	600
CATTAATTGC	GTTGCGCTCA	CTGCCGCTT	TCCAGTCGGG	AAAACGTGCG	TGCCACTGCN	660
TTANTGAATC	NGCCACCCCC	CGGGAAAAGG	CGGTTGCNTT	TTGGGCCTCT	TCCGCTTCC	720
TCGCTCATTG	ATCCTNGNC	CCGGTCTTCG	GCTGCGGNGA	ACGGTTCACT	CCTCAAAGGC	780
GGTNTNCCGG	TTATCCCCAA	ACNGGGGATA	CCCNGA			816

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAG	AAGGGATGGC	TGGGGTGT	TAAACAGCAGAG	GTGCAGGGCG	GGGGCTCACG	60
TCCTGCTCCT	CACTGGTGAT	AAACGAGCCC	CGTTCTTGT	TGTGATCATG	ATGAACAAACC	120

TCCTCAAAAG	TCAGAACCGG	AGTCACACAG	GCATCTGTGC	CGTCAAAGAT	TTGACACCAC	180
TCTGCCTTCG	TCTTCTTGC	AAATACATCT	GCAAACCTCT	TCTTCATTTC	TGGCCAATCA	240
TCCATGCTCA	TCTGATTGGG	AAGTTCATCA	GACTTTAGTC	CANNTCTTT	GATCAGCAGC	300
TCGTAGAAGT	GGGGTTCTAT	TGCTCCAACA	GCCATGAATT	CCCCATCTGC	TGTCCTGTAA	360
GTCGTATAGA	AAGGTGCTCC	ACCATCCAAC	ATGTTCTGTG	CTCGAGGGGG	GGCCCGGTAC	420
CCAATTGCC	CTATANTGAG	TCGTATTACG	CGCGCTCACT	GGCCGTCGTT	TTACAACGTC	480
GTGACTGGGA	AAACCCCTGGG	CGTTACCAAC	TTAATCGCCT	TGCAGCACAT	CCCCCTTTCG	540
CCAGCTGGGC	GTAATANCNA	AAAGGCCCGC	ACCGATGCC	CTTCCAACAG	TTGCGCACCT	600
GAATGGGNAA	ATGGGACCCC	CCTGTTACCG	CGCATTNAAC	CCCCGCNGGG	TTTNGTTGTT	660
ACCCCAACNT	NNACCGCTTA	CACTTTGCCA	GCGCCTTANC	GCCCCTCCCC	TTTCNCCTTT	720
CTTCCCTTCC	TTTCNCNCCN	CTTCCCCCG	GGGTTTCCCC	CNTCAAACCC	CNA	773

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCCCTCTCCT	120
TCGGAACACT	GGCTGTCTCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGAGATGGGA	GGGGTGGGGC	CCACCCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCT	360
GNNGGCACTG	GBAAGCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTTGT	CCCTTTAGTG	AGGGTTAAATT	480
GCGCCTTGG	CNTAATCATG	GTCATANCTN	TTTCCTGTGT	GAAATTGTTA	TCCGCTCACA	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCCCTTC	CAATCNGGAA	ACCTGTCTTG	660
CCNCTTGCAT	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	GTGGCGTTT	TGGCGCTCT	720
TCCGCTTCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTG	CGGCTGCNGC	AAACCGGTTG	780
ACCNCCCTCCA	AAGGGGTAT	TCCGGTTTCC	CCNAATCCGG	GGANANCC		828

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAG	TACTAACAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTT	AAAATTTGGT	TTTCATAAGA	TAATTTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240

ACATTTGGCA	TAAACAATAA	TAAAACAATC	ACAATTAAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATAA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	360
AATAGAACATC	CTTGGCCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTAC	TCAGCCCTGA	420
CATTCAAGTTT	TCAAAGTAGG	AGACAGGTTC	TACAGTATCA	TTTTACAGTT	TCCAACACAT	480
TGAAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTAAATG	CATTACATCC	TCAAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTC	AAAGTTATATT	AGTCATATAA	CTTGGTGTGCG	600
TTATTTTAAA	TTAGTGCTAA	ATGGATTAAG	TGAAGACAAAC	AATGGTCCCC	TAATGTGATT	660
GATATTGGTC	ATTTTACCA	GCTTCTAAAT	CTNAACTTTC	AGGCTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TGTTATTITG	TTAAAATTA	AATTAAACC	TGGTGAAAAA	ATAATTGAA	ATNA	834

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 818 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT	TTTTTTTTTT	AAGACCCTCA	TCAATAGATG	GAGACATACA	GAAATAGTCA	60
AACCACATCT	ACAAAATGCC	AGTATCAGGC	GGCGGCTTCG	AAGCCAAAGT	GATGTTTGGAA	120
TGTAAGTGA	AATATTAGTT	GGCGGATGAA	GCAGATAGTG	AGGAAAGTTG	AGCCAATAAT	180
GACGTGAAGT	CCGTGGAAGC	CTGTTGCTAC	AAAAAATGTT	GAGCCGTAGA	TGCCGTCGGA	240
AATGGTGAAG	GGAGACTCGA	AGTACTCTGA	GGCTTGTAGG	AGGGTAAAT	AGAGACCCAG	300
TAAAATTGTA	ATAAGCAGTG	CTTGAATTAT	TTGGTTTCGG	TTGTTTCTA	TTAGACTATG	360
GTGAGCTCAG	GTGATTGATA	CTCCTGATGC	GAGTAATACG	GATGTGTTTA	GGAGTGGGAC	420
TTCTAGGGGA	TTTAGCGGGG	TGATGCCTGT	TGGGGGCCAG	TGCCCTCCTA	GTTGGGGGGT	480
AGGGGCTAGG	CTGGAGTGGT	AAAAGGCTCA	AAAAAATCCT	GCGAAGAAAA	AAACTTCTGA	540
GGTAATAAT	AGGATTATCC	CGTATCGAAG	GCCTTTTTGG	ACAGGTGGTG	TGTGGTGGCC	600
TTGGTATGTG	CTTCTCGTG	TTACATCGCG	CCATCATTGG	TATATGGTTA	GTGTGTTGGG	660
TTANTANGGC	CTANTATGAA	GAACCTTTGG	ANTGGAATTA	AATCAATNGC	TTGGCCGGAA	720
GTCATTANGA	NGGCTNAAAA	GGCCCTGTAA	NGGGTCTGGG	CTNGGTTTTA	CCCNACCCAT	780
GGAATNCNCC	CCCCGGACNA	NTGNATCCCT	ATTCTTAA			818

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 817 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT	TTTTTTTTTT	TGGCTCTAGA	GGGGTAGAG	GGGGTGCTAT	AGGGTAAATA	60
CGGGCCCTAT	TTCAAAGATT	TTAGGGAA	TTAATTCTAG	GACGATGGGT	ATGAAACTGT	120
GGTTTGCTCC	ACAGATTCA	GAGCATTGAC	CGTAGTATAC	CCCCGGTCGT	GTAGCGGTGA	180
AAGTGGTTTG	GTAGACGT	CCGGAATTG	CATCTGTTT	TAAGCCTAAT	GTGGGGACAG	240
CTCATGAGTG	CAAGACGTCT	TGTGATGTA	TTATTATACN	AATGGGGCT	TCAATCGGGA	300

GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG	360
GAAGTATGTA GGAATTGAAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTAA	480
AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTTCCT GAAACGTCTG AAATGTTAAT AANAATTAAN TTNNGTTATT	600
GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG	660
CNTTATCCTN AAAGGTNATA ACCNCTCCTA TNATCCCACC CAATNGNATT CCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAAAANGGC CNCCCCCGG TGNANNCCNC CTTTGTTCC	780
CTTNANTGAN GGTTATTCNC CCCTNGCCTT ATCANCC	817

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120
CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCCTGGGG	240
TGGGTGGCCG ANGCCTGANC CGCTCTGCCT TGCTGCCCTT ANGTGGGCCG CCACCCCCCTG	300
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGGCGGACTT CAAGGANAAC CCCCACANGG	360
GGATTTTGCT CCTANANTAA GGCTCATCTG GGCCTCGGCC CCCCCCACCTG GTTGGCCTTG	420
TCTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTT NGGGAGTGT	480
CTCCTTACAA CCACANNATG CCCGGCTCCT CCCGGAAACC ANTCCCANCC TGNGAAGGAT	540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAAACC CNCTTNTGT	600
TCCTTTTCNT TNAGGGTTAA TNNGCCTTG GCCTTNCCAN NGTCCTNCNC NTTTCCNNT	660
GTTNAAATTG TTANGCNCCC NCCNNTCCCN CNNCNNCNAN CCCGACCCNN ANNTTNNANN	720
NCCTGGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT TGCNTTNGGG NNCCNTGCC	780
CTTCCCTCT NGGGANNCG	799

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCCACAT GATCCTTACT CTATGAGCAA	180
AATCCCTGT GGGGGCTCT CCTTGAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG	240
CAGGTCTATGG GGTTGTNGNC CAACTGGGGG CCNCAACGCA AAANGCNCA GGGCCTCNGN	300
CACCCATCCC ANGACGCGC TACACTNCTG GACCTCCCNC TCCACCACTT TCATGCGCTG	360

TTCNTACCCG CGNATNTGTC CCANCTGTT CNGTGCCNAC TCCANCTCT NGGACGTGCG	420
CTACATACGC CGGGANTCNC NCTCCCGCTT TGTCCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG ACCNATTCC CACNTTNNC AGNTTCCNC NNCGNGCTTC CTTNTAAAAG	540
GGTTGANCCC CGGAAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACTN CCCCCCTNATA	600
GCTGAANTCC CCATNACCCN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTTAA TCCCNCCTTG CNANGNNCNT CCCCCNNNTCC	720
NCCCNNTNG GCNTNTNANN CNAAAAAGGC CNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 789 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCAGGA GAAGCAGGTG TTCCTGCCCA	180
AATAACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG CCTGATGACC AGCTTCCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGTGGA GGCAGTGGCC	300
TGCTCCCACC TCCACCCCGCG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGTCTTC TGCTGTCCCA NGTGGCCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGTCG TCACTGCCTA TATGGTGTCT GCCGCAGGCC TGGGTCTGGT	540
CCCATTAACT TTGCTACACA GGTANTATTG GACAAGAACG ANTTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGTCC AACTCCCCGC	660
TCCGTGTAAC CCCATGGGGC TGCCGGCTTG GCCGCCAATT TCTGTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTTAAA TGCCTGTGTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGGTAA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTGTGTC TTGCCCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAAAATCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA GGTTAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAGCTC CCAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAAC	420

CTGAGCCTGG	GTAATCCACC	TGCAGAGTCC	CCGCATTCCA	GTGCATGGAA	CCCTTCTGGC	480
CTCCCCTGTAT	AAGTCCAGAC	TGAAACCCCC	TTGGAAGGNC	TCCAGTCAGG	CAGCCCTANA	540
AACTGGGAA	AAAAGAAAAG	GACGCCCAN	CCCCCAGCTG	TGCANCTACG	CACCTCAACA	600
GCACAGGGTG	GCAGCAAAAA	AACCACTTTA	CTTTGGCAC	AACAAAAACT	NGGGGGGGCA	660
ACCCCGGCAC	CCCNANGGGG	GTAAACAGGA	ANCNGGNAA	CNTGGAACCC	AATTNAGGCA	720
GGCCCNCAC	CCCNAATTNTT	GCTGGAAAT	TTTCCTCCC	CTAAATTNTT	TC	772

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATT	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCTC	TACTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCAC	GTCTCTTTG	180
AAGTANGGTG	AGTCCTCAAA	ATCCGTATAG	TTGGTGAAGC	CACAGCACTT	GAGCCCTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCTGGAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCA	GGAAAGTGTCTC	ACCCATTGTG	GTGTACACCA	AGGGGACAC	360
AGCAGCTGCN	ACCTCAGCAA	TGAAGATGAN	GAGGANGATG	AAGAAGAACG	TNCAGGGGC	420
ACACTTGCTC	TCAGTCTTAN	CACCATANCA	GCCCNTGAAA	ACCAANANCA	AAGACCACNA	480
CNCCGGCTGC	GATGAAGAAA	TNACCCCNCG	TTGACAAACT	TGCATGGCAC	TGGGANCCAC	540
AGTGGCCCN	AAAATCTTC	AAAAGGATGC	CCCATCNATT	GACCCCCAA	ATGCCCAC	600
CCAACAGGGG	CTGCCCCACN	CNCNNAAACGA	TGANCCNATT	GNACAAGATC	TNCNTGGTCT	660
TNATNAACNT	GAACCTGCGN	TNGTGGCTCC	TGTTCAAGGC	CNNGGCCTGA	CTTCTNAANN	720
AANGAACTCN	GAAGNCCCCA	CNGGANANN	G			751

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTGTCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTTCAGA	ACTCANTGCC	AAGANCCCTG	AAACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCATTTT	GCTCATCTTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCACTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTT	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATT	600

GAAGANTCAC CTACTTCAAA GAAAANAGTG CCTTTCCCCC ATTTCTGTTG CAATTGACAA	660
ACGTCCCCAA CACAGCCAAT TGAAAACCTG CACCCAAACCC AAANGGGTCC CCAACCANAA	720
ATTNAAGGG	729

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT CAAAGTTGTT CTTGTTGCCA TAACAACCAC CATAGGTAAA GCGGGCGCAG	60
TGTTCGCTGA AGGGGTTGTA GTACCAGCGC GGGATGCTCT CCTTGCAGAG TCCTGTGTCT	120
GGCAGGTCCA CGCAGTGCCC TTTGTCACTG GGGAAATGGA TGCGCTGGAG CTCGTCAAAG	180
CCACTCGTGT ATTTTTCACA GGCAGCCTCG TCCGACGCGT CGGGGCAGTT GGGGGTGTCT	240
TCACACTCCA GGAAACTGTC NATGCAGCAG CCATTGCTGC AGCGGAACGT GGTGGCTGA	300
CANGTGCAG AGCACACTGG ATGGCGCTT TCCATGNNA GGGCCCTGNG GGAAAGTCCC	360
TGANCCCCAN ANCTGCCTCT CAAANGCCCC ACCTTGACACA CCCCGACAGG CTAGAATGGA	420
ATCTTCTTCC CGAAAGGTAG TTNTTCTTGT TGCCCAANCC ANCCCNNTAA ACAAACTCTT	480
GCAANATCTGC TCCGNGGGGG TCNTANTACC ANC GTGGGAA AAGAACCCCA GGCNGCGAAC	540
CAANCTTGTG TGGATNCGAA GCNATAATCT NCTNTTCTGC TTGGTGGACA GCACCANTNA	600
CTGTNNANCNT TTAGNCCNTG GTCCTCNTGG GTTGNNCTTG AACCTAATCN CCNNNTCAACT	660
GGGACAAGGT AAANTNGCCNT CCTTTNAATT CCCNANCNTN CCCCCTGGTT TGGGGTTTTN	720
CNCNCTCCTA CCCCAGAAA NCCGTGTTCC CCCCCAACTA GGGGCCNAAA CCNNTTNTTC	780
CACAACCCTN CCCCACCCAC GGGTTCNGNT GGTTNG	816

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG GGCAGGCATA NACTTGAAGG TACAACCCCA GGAACCCCTG GTGCTGAAGG	60
ATGTGGAAAA CACAGATTGG CGCCTACTGC GGGGTGACAC GGATGTCAGG TAGAGAGAGGA	120
AAGACCCAAA CCAGGGGAA CTGTGGGGAC TCAAGGAANG CACCTACCTG TTCCAGCTGA	180
CAGTGACTAG CTCAGACCCAC CCAGAGGACA CGGCCAACGT CACAGTCACT GTGCTGTCCA	240
CCAAGCAGAC AGAAGACTAC TGCCCTCGCAT CCAACAANGT GGGTCGCTGC CGGGGCTCTT	300
TCCCACGCTG GTACTATGAC CCCACGGAGC AGATCTGCAA GAGTTTCGTT TATGGAGGCT	360
GCTTGGGCAA CAAGAACAAAC TACCTTCGGG AAGAAGAGTG CATTCTANCC TGTCNGGGTG	420
TGCAAGGTGG GCCTTTGANA NGCANCTCTG GGGCTCANGC GACTTTCCCC CAGGGCCCCCT	480
CCATGGAAAG GCGCCATCCA NTGTTCTCTG GCACCTGTCA GCCCACCCAG TTCCGCTGCA	540
NCAATGGCTG CTGCATCNAC ANTTTCCTNG AATTGTGACA ACACCCCCCA NTGCCCCCAA	600
CCCTCCCAAC AAAGCTTCCC TGTTNAAAA TACNCCANTT GGCTTTTNAC AACCNCCCAG	660
CNCCTCCNTT TTCCCCNNNTN AACAAAGGGC NCTNGCNTTT GAACTGCCCN AACCCNGGAA	720

TCTNCCNNNGG AAAAANTNCC CCCCTGGTT CCTNNAANCC CCTCCNCNAA ANCTNCCCCC CCC	780
	783

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCAATT CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTCGGAT GTCATACAAA AGCTGATTGA AGCAACCCTC TACTTTTG TGCGAGCCT TTTGCTTGGT GCAGGTTTCA TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCAGT GTTCTCTTTG AAGTAGGGTG AGTCCTCAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTTC ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA GCCACTACCA GCAACGTCAG GAAGTGCTCA GCCATTGTGG TGTACACCAA GGCACCCACA GCAGCTGCAA CCTCAGCAAT GAAGATGAGG AGGAGGATGA AGAAGAACGT CNCGAGGGCA CACTTGCTCT CCGTCTTAGC ACCATAGCAG CCCANGAAAC CAAGAGCAAA GACCACAACG CCNGCTGCGA ATGAAAGAAA NTACCCACGT TGACAAACTG CATGGCCACT GGACGACAGT TGGCCCGAAN ATCTTCAGAA AAGGGATGCC CCATCGATTG AACACCCANA TGCCCACACTGC CNACAGGGCT GCNCCNCNC GAAAGAATGA GCCATTGAAG AAGGATCNTC NTGGTCTTAA TGAAGTAAA CCNTGCATGG TGGCCCTGT TCAGGGCTCT TGGCAGTGAA TTCTGANAAA AAGGAACNGC NTNAGCCCC CCAAANGANA AAACACCCCC GGGTGTGCC CTGAATTGGC GGCCAAGGAN CCCTGCCCCN G	60 120 180 240 300 360 420 480 540 600 660 720 780 801
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## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA GGCGTCCCTC TGCCTGCCA CTCAGTGGCA ACACCCGGGA GCTGTTTGT CCTTGTGGA GCCTCAGCAG TTCCCTCTTT CAGAACTCAC TGCCAAGAGC CCTGAACAGG AGCCACCATG CAGTGCCTCA GCTTCATTAA GACCATGATG ATCCCTCTCA ATTTGCTCAT CTTTCTGTGT GGTGCAGCCC TGTTGGCAGT GGGCATCTGG GTGTCAATCG ATGGGGCATC CTTTCTGAAG ATCTTCGGGC CACTGTCGTC CAGTGCCTATG CAGTTGTCA ACGTGGCTA CTTCCTCATC GCAGCCGGCG TTGTGGTCTT TGCTCTTGGT TTCCTGGCT GCTATGGTGC TAAGACGGAG AGCAAGTGTG CCCTCGTGCAC GTTCTTCTTC ATCCCTCTCC TCATCTTCAT TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCAATTCT GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTCCCC AACTATACCG GAATTTGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCCTTNCC CCCNTCTGT TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNAAA CAAAAAAANT NNAAGGGTTN	60 120 180 240 300 360 420 480 540 600 660 720 740
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## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA	60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG	120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT	180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCCT	240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA	300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT	360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT	420
GGTTCTGCCCG TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG	480
GCTCAGGATG TCCAGAGACG TGGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC	540
GTCGGCTCCC GCGCANTGNG TTCGTCGTNC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC	600
AANCTTCGTC NGGCCCATGG AATTCAACNC ACCGGAACTN GTANGATCCA CTNNTTCTAT	660
AACCGGNCGC CACCGCNNT GGAACTCCAC TCTTNTTNCC TTTACTTGAG GGTAAAGGTC	720
ACCCTTNNCG TTACCTTGGT CCAAACCNNT CCNTGTGTGCG ANATNGTNAA TCNGGNCCNA	780
TNCCANCCNC ATANGAAGCC NG	802

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC AGGTNACGGG CGCGNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG	60
GAGCCCACCG TCACGNGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT	120
CNTGACCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG	180
CAGGAACCAA GANCAAANN C TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC	240
GCNCATCCNT CNAGTGTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGCENNNGA	300
CATGCCAGN GTTANATAAC NGGCGAGAG TNANNTTGCC TCTCCCTTCC GGCTGCGCAN	360
CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT	420
CCACTAAGCT CAGAACAAAA AACCTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA	480
AAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG	540
GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC	600
CNNCNNTCCA AGGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN	660
CCCCNGGCC CGGCCTTTA CNANCNTCNN NNACNGGNA AAACCNNGC TTTNCCCAAC	720
NNAATCCNCC T	731

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTT	TTTTTTTTT	AAAAACCCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCC	CTC	NTCCAAATNN	CCNTTCCGG	GNGGGGGTTC	CAAACCCAAN	120
ANNTTAAATT	AAATNTTNNT	TGGGGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNAA	TNCCTGGAAA	CCNGTNGNTT	CCAAAAATNT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTNGCCAC	GCCTGAATT	ATTGGNTTCC	GNTGTTTCC	NTAAAAANAA	360
GGNNANCC	GGTTANTNAA	TCCCCCN	CCCAATTATA	CCGAN	TTNGAATTG	420
GANCCCN	CGG	GAATTAACGG	GGNNNNNTCCC	TNTTGGGGG	CNGGNNCCCC	480
GGTTNGGGNC	AGGN	NCNAAT	TGTTAAGGG	TCCGAAAAT	CCCTCCNAGA	540
CCAGGNTGAG	NNTNGGGTT	NCCCCCCCCC	CANGGCCCT	CTCGNANAGT	TGGGGTTTG	600
GGGGCCTGGG	ATTTNTTTC	CCCTNTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCN	NC	AGANCTTTN	CCGANTTNAN	TTAAATCCNT	GCCTNGGC	720
AGTCCNTTGN	AGGGNTAA	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCNC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNN	TTN	NATCACNCCC	CNCCNACTAC	GCCCNCNANC	120
NNCANATNCC	ACTGAN	NGCG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	180
CCAGCTGTCC	NANAANGC	CCT	NNNATACNGG	NNNATCCAAT	NTGNANCC	240
NNCNCN	AN	CCGATTAC	CCNTNCCCC	TANCCCCTCC	CCCCAACNA	300
CGAAGGCN	CT	GGNCCNAAGG	NNGCCNCNCC	CCGCTAGNTC	CCCNCAAGT	360
AACTCANCN	NATTACNC	GC	TTCNTGAGTA	TCACTCCCCG	AATCTCACCC	420
AAAAANATCN	GATA	CAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	480
TTAGNGGTCC	NTNA	ANCNTC	CTAATAC	TTTC	GGTCTCTATT	540
CTTCNGACA	GCAT	NTTTG	CAGTCTN	TCNCC	CCNAANGG	600
GGGCTCNTCT	TTTC	CTTCGG	TTAN	CCGG	TTCTNGAAC	660
AAATTCNTNC	CNTT	TANTTT	TGGC	CCNA	AACCCCCGGC	720
AAAAGGTTGT	TTTG	ANAAAA	TTTT	CTTG	CTTGAAAACG	755

(2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT	TTTTTANGTG	TNGTCGTGCA	GGTAGAGGCT	TACTACAANT	GTGAANACGT	60
ACGCTNGGAN	TAANGCGACC	CGANTTCTAG	GANNCCNCCCT	AAAATCANAC	TGTGAAGATN	120
ATCCTGNNA	CGGAANGGTC	ACCGGNNNGAT	NNTGCTAGGG	TGNCCNCTCC	CANNNCNTTN	180
CATAACTCNG	NGGCCCTGCC	CACCACTTC	GGCGGCCCNNG	NGNCCGGGCC	CGGGTCATTN	240
GNNTTAACCN	CACTNNGCNA	NCGGTTCCN	NCCCCNNCNG	ACCCNNGCGA	TCCGGGGTNC	300
TCTGTCTTCC	CCTGNAGNCN	ANAAANTGGG	CCNCGGNCCC	CTTTACCCCT	NNACAAGCCA	360
CNGCCNTCTA	NCCNCNGCCC	CCCCTCCANT	NNGGGGGACT	GCCNANNGCT	CCGTTNCTNG	420
NNACCCCN	GGGTNCCTCG	GTTGTCGANT	CNACCGNANG	CCANGGATTG	CNAAGGAAGG	480
TGCGTTNTTG	GCCCCTACCC	TTCGCTNCGG	NNCACCCCTTC	CCGACNANGA	NCCGCTCCCG	540
CNCNNCGNN	CCTCNCTCG	CAACACCCGC	NCTCNTCNGT	NCGGNNNCCC	CCCCACCCGC	600
NCCCTNCNC	NGNCGNANCN	CTCCNCCNCC	GTCTCANNCA	CCACCCCGCC	CCGCCAGGCC	660
NTCANCCACN	GGNNGACNNG	NAGCNCNNTC	GCNCCGCGCN	GCGNCNCCT	CGCCNCNGAA	720
CTNCNTCNGG	CCANTNNCGC	TCAANCCNNA	CNAAACGCCG	CTGCGGGCC	CGNAGCGNCC	780
NCCTCCNCGA	GTCCTCCCGN	CTTCCNACCC	ANGNNNTCCN	CGAGGACACN	NNACCCGCC	840
NNCANGCGG						849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA	TACTTCGCTC	GNACTCGTGC	GCCTCGCTNC	TCTTTCCCTC	CGCAACCATG	60
TCTGACNANC	CCGATTNGGC	NGATATCNAN	AAGNTCGANC	AGTCCAAACT	GANTAACACA	120
CACACNCNAN	AGANAAATCC	NCTGCCTTCC	ANAGTANACN	ATTGAACNNG	AGAACCCANGC	180
NGGCGAATCG	TAATNAGGCG	TGCGCCGCCA	ATNTGTCNCC	GTTTATTNTN	CCAGCNTCNC	240
CTNCCNACCC	TACNTCTTCN	NAGCTGTCNN	ACCCCTNGTN	CGNACCCCCC	NAGGTGGGGA	300
TCGGGTTTNN	NNTGACCGNG	CNNCCCTCC	CCCCNTCCAT	NACGANCCNC	CCGCACCACC	360
NANNGCNCG	NCCCCGNNCT	CTTCGCCNCC	CTGTCCNTN	CCCCCTGTNGC	CTGGCNCNGN	420
ACCGCATTGA	CCCTCGCCNN	CTNCNNGAAA	NCGNANACGT	CCGGGTTGNN	ANNANCGCTG	480
TGGGNNNGCG	TCTGCNCCGC	GTTCCTTCCN	NCNNCTTCCA	CCATCTTCNT	TACNGGGTCT	540
CCNCGCCNTC	TCNNNCACNC	CCTGGGACGC	TNTCCTNTGC	CCCCCTTNAC	TCCCCCCCTT	600
CGNCGTGNCC	CGNCCCCACC	NTCATTNCA	NACGNTCTTC	ACAANNNCCT	GGNTNNCTCC	660
CNANCNGNCN	GTCANCCNAG	GGAAAGGGNGG	GGNNCCNNTG	NTTGACGTTG	NGNGANGTC	720
CGAANANTCC	TCNCNTCAN	CNCTACCCCT	GGGGCGNNCT	CTCNGTTNCC	AACTTANCAA	780
NTCTCCCCCG	NGNGCNCNTC	TCAGCCTCNC	CCNCCCCNCT	CTCTGCANTG	TNCTCTGCTC	840
TNACCNNTAC	GANTNTTCGN	CNCCCTCTTT	CC			872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATAACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA	120
TCNTNCATTA GTAACAANTG TNNTGTCCAT CCTGTCNGAN CANATTCCCA TNNAATTNCGN	180
CGCATTNCNC GCNCANTATN TAATNGGGAA NTCNNNTNNN NCACCCNNCAT CTATCNTNCC	240
GCNCCCTGAC TGGNAGAGAT GGATNANTTC TNNTNTGACC NACATGTTCA TCTTGGATTN	300
AANANCCCCC CGCNGNCCAC CGGTTNGNNG CNAGCCNNTC CCAAGACCTC CTGTTGGAGGT	360
AACCTGCGTC AGANNCATCA AACNTGGAA ACCCGCNMCC ANGTTNAAGT NGNNNCANAN	420
GATCCCCTGCC AGGNTTNACC ATCCCTTCNC AGCGCCCCCT TTNGTGCCTT ANAGNGNAGC	480
GTGTCCNANC CNCTCAACAT GANACGCGCC AGNCCANCCG CAATTNGCA CAATGTCGNC	540
GAACCCCCCTA GGGGGANTNA TNCAAANCCC CAGGATTGTC CNCNCANGAA ATCCCNCANC	600
CCCNCCCTAC CCNNCTTGG GACNGTGACC AANTCCCGGA GTNCCAGTCC GGCGNGNCTC	660
CCCCACCGGT NNCCNTGGGG GGGTGAANCT CNGNNTCANC CNGNCAGGN NTCGNAAGGA	720
ACCGGNCTN GNCGAANNG ANCNCNTNGA AGNGCCNNT CGTATAACCC CCCCTCNCCA	780
NCCNACNGNT AGNTCCCCCCC CNGGGTNCGG AANGG	815

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 775 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC TCGCTCCGTG GCCTTAGCTG TGCTCGCGCT ACTCTCTCTT TCTGGCCTGG	60
AGGCTATCCA GCGTACTCCA AAGATTCAAGG TTTACTCAGC TCATCCAGCA GAGAATGGAA	120
AGTCAAATTT CCTGAATTGC TATGTGTCTG GGTTTCATCC ATCCGACATT GAANTTGACT	180
TACTGAAGAA TGGANAGAGA ATTGAAAAAG TGGAGCATTC AGACTTGTCT TTCAGCAAGG	240
ACTGGTCTTT CTATCTCNG TACTACACTG AATTCAACCC CACTGAAAAA GATGAGTATG	300
CCTGCCGTGT GAACCATGTG ACTTTGTAC AGCCCAAGAT AGTTAAGTGG GATCGAGACA	360
TGTAAGCAGN CNNCATGGAA GTTTGAAGAT GCCGCATTG GATTGGATGA ATTCAAATT	420
CTGCTTGCTT GCNTTTTAAT ANTGATATGC NTATACACCC TACCCTTAT GNCCCCAAAT	480
TGTAGGGTT ACATNANTGT TCNCNTNGGA CATGATCTTC CTTTATAANT CCNCNTTCG	540
AATTGCCGT CNCCNGTTN NGAATGTTTC CNNAACCAGC GTTGGCTCCC CCAGGTCNCC	600
TCTTACGGAA GGGCCTGGGC CNCTTNCAA GGTTGGGGGA ACCNAAAATT TCNCTNTGC	660
CCNCCCNCCA CNNTCTTGNG NNCNCANTTT GGAACCCTTC CNATTCCCCT TGGCCTCNNA	720
NCCTNNCTA ANAAAATTN AAANGTNGC NAAAANNNTTN ACTTCCCCCCC TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 820 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC AGTGTAATCT TTTCCCAGAG GTGTGTANAG GGAACGGGGC CTAGAGGCAT	60
CCCANAGATA NCTTATANCA ACAGTGCTT GACCAAGAGC TGCTGGGCAC ATTTCCGTGCA	120
GAAAAGGTGG CGGTCCCCAT CACTCCTCCT CTCCCATAGC CATCCCAGAG GGGTGGAGTAG	180
CCATCANGCC TTCGGTGGGA GGGAGTCANG GAAACAACAN ACCACAGAGC ANACAGACCA	240
NTGATGACCA TGGGCGGGAG CGAGCCTCTT CCCTGNACCG GGGTGGCANA NGANAGCCTA	300
NCTGAGGGGT CACACTATAA ACGTTAACGA CCNAGATNAN CACCTGCTTC AAGTGCACCC	360
TTCCCTACCTG ACNACCAGNG ACCNNNAACT GCNGCCTGGG GACAGCNCTG GGANCAGCTA	420
ACNNAGCACT CACCTGCCCT CCCATGGCCG TNCGCNTCCC TGGTCCTGNC AAGGGAAGCT	480
CCCTGTTGGA ATTNCGGGGA NACCAAGGGGA NCCCCCTCCT CCANCTGTGA AGGAAAAAANN	540
GATGGAATTG TNCCCTTCCG GCCNNTCCCC TCTTCCTTTA CACGCCCTT NNTACTCNTC	600
TCCCTCTNTT NTCCGNNCNC ACTTTTNACC CCNNNATTTC CCTTNATTGA TCGGANCTN	660
GANATTCCAC TNNCGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT	720
GGGNNCCTCG NTCATCCTCT CTTTTCNCT ACCNCCNNTT CTTTGCCTCT CCTTNGATCA	780
TCCAACCNTC GNTGGCCTNT CCCCCCCNNN TCCTTNCCTC	820

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT GGCTCTTCC TCCTCAGGGGA CCTCTGACTG CTCTGGCCA AAGAATCTCT	60
TGTTTCTTCT CCGAGCCCCA GGCAGCGGTG ATTCAAGCCCT GCCCCAACCTG ATTCTGATGA	120
CTGCGGATGC TGTGACGGAC CCAAGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGCGC	180
CTGCTGAGCA CTTCCGCCCTC TCACCCCTGCC CAGCCCCCTGC CATGAGCTCT GGGCTGGGTC	240
TCCGCCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGGG CCACACTGGC	300
TTCTTCCTGC CCCNTCCCTG GCTCTGANTC TCTGTCTTCC TGTCTGTGC ANGCNCCTTG	360
GATCTCAGTT TCCCTCNCTC ANNGAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT	420
TATNACCNAN TGGNCTGTNC TGTCCNACTT TAATGGGCCN GACCGGCTAA TCCCTCCCTC	480
NCTCCCTTCC ANTTCNNNA ACCNGCTTNC CNTCNCTCC CCNTANCCCG CCNNGGAANC	540
CTCCTTGCCTC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGCNG GTNNCTNCNC	600
CTGNTNNCCC CNCTCNNTN TNCCCTGTC C NNCCNNCGCN NNGCANNTTC NCNGTCCNN	660
TNNCTCTCN NGNTCGNA NGNTCNCTN TNNNNNNGCN NGNTNNNTNC TCCCTCTCNC	720
CNNNTGNANG TNNTNNNNNC NCNGNNCCCC NNNNCNNNNN NGGNNTNNN TCTNCNCNGC	780
CCCNCCCCCCC NGNATTAAGG CCTCCNNCTC CGGGCCNC	818

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

## (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAAGG AGNATAANGG GGGAGGTGTG	60
TCCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTANN CCNGGTGGGT	120
GATTNAACCC CATTGTATGG AGNAAAGGN TTNAGGGAT TTTTCGGCTC TTATCAGTAT	180
NTANATTCT GTNAATCGGA AAATNATNTT TCNNCNGAA AATNTGCTC CCATCCGNAA	240
ATTNCTCCCG GGTAGTCAT NTTNGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT	300
ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNAC AGAGNATCCN TACCCGACTG	360
TNNNTTNCCCT TCGCCCTNTG ACTCTGCNNAGGCCAATAC CCNNNGNGNAT GTCNCCNGN	420
NNNGCGNCNC TGAAANNNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAAGCNN	480
CGTTTCNCAT NAAGGCACTT TNGCCTCATC CAACCNCNTG CCCTCNCCCA TTTNGCCGTC	540
NGGTTTCNCCT ACGCTNNNTG CNCCTNNTN GANATTTCNC CCGCCTNGGG NAANCCTCCT	600
GNAATGGGTA GGGNNTNTC TTTTNACCNN GNGGTNTACT AATCNCTNC ACCCNTNCTT	660
TCTCNACCCC CCCCCTTTTT CAATCCCANC GGCAATGGG GTCTCCCN CGANGGGGGG	720
NNNCCCANNC C	731

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGNNCNC TTCTATGANT ANTNTTAGAT	60
CGCTCANACC TCACANCCTC CCNACNANGC CTATAANGAA NANNAATAGA NCTGTNCNNNT	120
ATNTNTACNC TCATANNCTT CNNNACCCAC TCCCTCTTAA CCCNTACTGT GCCTATNGCN	180
TNNCTANTCT NTGCCGCCTN CNANCCACCN GTGGGCCNAC CNCNNGNATT CTCNATCTCC	240
TCNCCATNTN GCCTANANTA NGTNACATACC CTATAACCTAC NCCAATGCTA NNNCTAACNC	300
TCCATNANTT ANNNTAACTA CCACTGACNT NGACTTTCCNC ATNACNTCCT AATTGAAATC	360
TACTCTGACT CCCACNGCCT ANNNATTAGC ANCNTCCCCC NACNATNTCT CAACCAAATC	420
NTCAACAACC TATCTANCTG TTCNCCAACC NTTNCCTCCG ATCCCCNNAC AACCCCCCTC	480
CCAATACCC NCCACCTGAC NCCTAACCCN CACCATCCCG GCAAGCCNAN GGNCAATTAN	540
CCACTGGAAT CACNATNGGA NAAAAAAAAC CCNAACTCTC TANCNCNNAT CTCCCTAANA	600
AATNCTCCTN NAATTCTACT NCANTNCCAT CAANCCACN TGAAACNNAA CCCCTGTTTT	660
TANATCCCTT CTTTCGAAAA CCNACCCCTT ANNNCCCAAC CTTTNGGGCC CCCCCNCTNC	720
CCNAATGAAG GNCNCCCAAT CNANGAAACG NCCNTGAAAA ANCAGGCNA ANANNNTCCG	780
CANATCCTAT CCCTTANTTN GGGGNCCCTT NCCCNNGGCC CC	822

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AA GTGATGGA	CTGCCCATTG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCCTT	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCCCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGCC	TCTCTCGCCA	GCCTCCCCCT	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTGT	420
TCCCNTTAAT	GAAGGTTAAT	TGCNCGCTT	GCGTAATCAT	NGGTCANAAC	TNTTTCCTGT	480
GTGAAATTGT	TTNTCCCTC	NCNATTCCNC	NCNACATAACN	AACCCGGAAN	CATAAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGCGTT	GGCTCATGGC	600
CCGCTTCCN	TTCNGGAAAA	CTGTCNTCCC	CTGCNTNNNT	GAATCGGCCA	CCCCCCNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCCT	CCNCTCCCC	CCTCNCATAAN	CCCTNCGCCT	720
CGGTGTTNC	NGGTNGCGGG	GAANGGNAT	NNNCTCCNC	NAAGGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTT	TTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTTGGGG	GTGTGTGTAC	60
CATGTACCAAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNCACANATC	CCTACGATTTC	TTGACACCTG	GATTTCACCA	300
GGGGACCTTC	TGTTCTCCCA	NGGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNTCNAAN	AAGTAATTCA	CCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAACT	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCNN	CCTGAANGCG	CCAAGTTGAA	AGGCCACGCC	GTNCCNCTC	CCCATAGNAN	600
NTTTTNNCCT	CANCTAATGC	CCCCCCNGGC	AACNATCCAA	TCCCCCCCN	TGGGGGCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CGCANNNNNN	NGGTNNCNAC	780
CTCGCCCCCCC	CCNNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTA	TTGACAACCT	CNCGGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GCGCGGCGG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCCT	CTGCAGCTGC	AGGATGCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTNN	AATTCCACG	GGCACAAATGC	GGTCGCANCC	CCTCACCAACC	300
NATTAGGAAT	AGTGGTNNTA	CCCNCCNCCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GGGGCTCCGG	CATCTGGTCT	AAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAACCC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCCN	AAAAAAANC	CCGGGGGGNC	CCAGTTTCAA	CAAAGTCATC	600
CCCTTGCC	CCCAAATCCT	CCCCCGNTT	NCTGGGTTTG	GGAACCCACG	CCTCTNNCTT	660
TGGNNGGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGGTGGGC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCCC	NNGNNACGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
		CCCCCCNCG				789

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATT CATGGC	TGTTGGAGCA	ATANAACCCC	AGTTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GA C TAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAATGAANA	180
AGAAGTTGC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300
ACAANGAACG	GGGCTCGTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCA	GCCATCCCTT	CTTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	GCGGTGGAGC	TCCAGCTTTT	GTTCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAAGC	ATNAAATTTT	AAAGCCTGGN	GGTNGCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTTCC	AGTCCGGAAA	ACCTGTCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGGGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCTGAANT	CCTTCCCCCC	GGTCTTCGG	CTTGCAGCNA	780
ACGGTATCNA	CCT					793

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGGA	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGC	GGGAANAGCT	GGGTCGACTC	AAGCTAGTT	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAAGCT	GACCAAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CTTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTCTTGG	GCCTCAACCT	CCTCTTCCCTG	CTGTCCCGAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCGGCTGCC	TGCCCAANGA	CATACANACC	AATGTCTACA	TCNACCACCA	420
GTGTCCTGGA	GCAATACTGA	TGGANGGCAG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTCA	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAACATCG	GCCCCGCCATC	GCGGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAAAT	TCCACGCCNA	CATTNG			756

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGAA	GCTCTCGGCT	GCTGTNTTTA	AGTTGCTCAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAAACAN	CAGGATNTGA	GTCTTGATTT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAACTC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCCT	TGGTGAACCTC	CCCTTCAAAG	TTGTTCCGGC	CTTCATCAAA	300
CTTCTNNAAAN	ANGANNANCC	CANCTTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAACTGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGCNCAAATC	CGACTCCCCN	TCCTTGAAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNCCNNG	CAGGGTTGGT	GGCANNCGG	GCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGGG	600
GGAAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCCNT	660
ACNTNCTGGG	CCGGGTTCAA	ANTCCCTCCN	TTGNCNNTCN	CCTCGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCTTCCCC	CNCCCCNCGG	NGTTTGGNTT	TTTCATNGGG	CCCCAACTCT	780
GCTNTTGGCC	ANTCCCTGG	GGGCNTNTAN	CNCCCCCTNT	GGTCCCNNTNG	GGCC	834

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNCGCTTT	CCNGCCGCGC	CCCGTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAG	GAAGAAAGGC	TGGTCTCTCC	ACCCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAA	AAAAATAAAC	AANAGGTTT	GTTCTCATGG	CTGCCAACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGCTT	GANAATATT	CTTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCC	ACNTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAGGCCTGAA	NCTTAGTCTC	CAAAAGTCTC	NGCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNNCAGTG	GATCTGCCAA	ANANTACCN	TATCATCNNT	GAATAAAAAG	540
GCCCCCTGAAC	GANATGCTTC	CANCANCCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCCCT	GGGTCCCANT	CCCTCCCTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCCTGGC	720
ATTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAACCA	CNCN			814

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAAA	GTTGTTCTTG	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
CGCGAGTGT	CGCTGAAGGG	GTTGTAGTAC	CAGCGGGGA	TGCTCTCC	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTTG	TCACTGGGA	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCGTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTGTCAC	ACTCCACTAA	ACTGTGATN	CANCAGCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGCTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCTTNANCC	CAAAC TGCTC	CTCAAAGGCC	ACCTTGACACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCCAAGCA	NCCTCCANCA	AACCAAAANC	480
TTGAAAATC	TGCTCCGTGG	GGGTCACTNNN	TACCANGTT	GGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTTTGAATGC	NAAGGNAATA	ATCCTCCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAACT	GTAAACNTG	GGCCGNGTTC	CNCTNGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAA	GGTANGTGCC	TTCCTGAAAT	TCCCAAANTT	CCCCTNGNTT	TGGGTNNNTT	720
CTCCTCTNCC	CTAAAATCG	TNTTCCCCCC	CNTANGGCG			760

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTAAAAA	CCCCCTCCAT	TGAATGAAAA	60
CTTCCNAAAT	TGTCCAACCC	CCTCNCCAA	ATNNCCATT	CGGGGGGGG	GTTCCAAACC	120

CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGG AANAANCAA ATGTNAAGAA	180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTNTTAACC	240
CTTAAATCCC TCCGAAATTG NTAANGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT	300
NGATTTAACC CCCCTTNANT TNTTTTNACC CNNGNCTNA NTATTTNGNT TCCGGTGT	360
TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNNCCT AANCCAATTA AACCGAATT	420
TTTTGAATT GGAAATTCCN NGGAATTNA CGGGGTTTT TCCCNNTTG GGCCATNCC	480
CCCNNTTCG GGGTTGGGN NTAGGGTGA TTTTNNANG NCCCAAAAAA NCCCCAANA	540
AAAAAAACTCC CAAGNNTAA TTNGAATNTC CCCCTTCCCA GGCCTTTGG GAAAGGNGG	600
TTNTGGGGG CCNGGGANTT CNTTCCCCN TTCCNCCCC CCCCCNGGT AAANGTTAT	660
NGNNNTTGGT TTTGGGCC CTTNANGAC CTTCCGGATN GAAATTAAT CCCGGGNCG	720
GCCG	724

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT TTTTCTTG CTCACATTAA ATTNTTATTT TGATTTTTT TAATGCTGCA	60
CAACACAATA TTTATTTCAT TTGTTCTTT TATTTCATTT TATTTGTTG CTGCTGCTGT	120
TTTATTTATT TTTACTGAAA GTGAGAGGGA ACTTTGTGG CCTTTTTTCC TTTTCTGTA	180
GGCGCCCTTA AGCTTTCTAA ATTTGAAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT	240
CGAAAATCA CTCGGGGAA NGGAAGGTT GCCTTGTAA TCATGCCCTA TGGTGGGTGA	300
TTAACTGCTT GTACAATTAC NTTCACTTT TAATTAATTG TGCTNAANGC TTTAATTANA	360
CTTGGGGGTT CCCTCCCCN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG	420
TCCCCGCNNT CNTGAAACA CACNGCNGAA NGTTCTCATT NTCCCNCCNC CAGGTAAAAA	480
TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCNM GCCTGAATCC TCNAAAANCN	540
CCCTCAANCN AATTNCTNNG CCCCGTCNC GCNTNNGTCC CNCCCGGGCT CGGGAANTN	600
CACCCCCNGA ANNCNNNTNC NAACNAAATT CGAAAATAT TCCCNNTCNC TCAATTCCCC	660
CNNAGACTNT CCTCNCNAN CNCAATTTC TTTTNTCAC GAACNCNNC CNNAAAATGN	720
NNNNCNCCN CNTNGTCCN NAATCNCCN C	751

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTGGTATTCTT CTGTAAGATC AGGTGTTCC CTCTCGTAGG TTTAGAGGAA ACACCCCTCAT	60
AGATGAAAAC CCCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGG GTAGGAGGG	120
CGCCCTATGC ACAGCTGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA	180
TGGTCTGGAA GCGGCGGCTG TACCTGCGTA GGGGCACACC GTCAGGGCCC ACCAGGAACT	240
TCTCAAAGTT CCAGGCAACN TCGTTGCGAC ACACCGGAGA CCAGGTGATN AGCTTGGGT	300

CGGTCATAAN CGCGGTGGCG TCGTCGCTGG GAGCTGGCAG GGCTCCGC AGGAAGGCNA	360
ATAAAAGGTG CGCCCCCGCA CCGITCANCT CGCACTTCTC NAANACCATG ANGTTGGGCT	420
CNAACCCACC ACCANNCCCG ACTTCCTTGA NGGAATTCCC AAATCTCTTC GNTCTTGGC	480
TTCTNCTGAT GCCCTANCTG GTTGCCCNGN ATGCCAANCA NCCCCAANCC CCGGGGTCT	540
AAANCACCCN CCTCCTCMTT TCATCTGGGT TNTTNNTCCCC GGACCNTGGT TCCTCTCAAG	600
GGANCCCAT A TCTCNACCAN TA TCTCACCN NT NCCCCCNNT GNNACCCANC CTTCTANNGN	660
TTCCCNCNG NCCTCTGGCC CNTCAAANAN GCTTNCACNA CCTGGGTCTG CCTTCCCCCC	720
TNCCCTATCT GNACCCCN CN TTTGTCTCAN TNT	753

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA TCACAACAGA CATGCTTCAT CCCATAGACT TCTTGACATA GCTTCAAATG	60
AGTGAACCCA TCCTTGATT T ATATACATAT ATGTTCTAG TATTTGGGA GCCTTCCAC	120
TTCTTAAAC CTTGTTCA TT ATGAACTG AAAATAGGAA TTTGTGAAGA GTTAAAAAGT	180
TATAGCTTGT TTACGTAGTA AGTTTTGAA GTCTACATTC AATCCAGACA CTTAGTTGAG	240
TGTTAAACTG TGATTTTAA AAAATATCAT TTGAGAATAT TCTTCAGAG GTATTTCAT	300
TTTTACTTTT TGATTAATTG TGTTTTATAT ATTAGGGTAG T	341

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 101 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA TTTAGTTCTG TGCTCTTCCT TATTTAGTGT TGTATCATAA ATACTTGAT	60
GTTTCAAACA TTCTAAATAA ATAATTTCAT GTGGCTTCAT A	101

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTCCTG GTCCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCACTAAA GAGGAATTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAAATAT CAGAGAAAAG TAGTCTTGA AATATTTACG TCCAGGAGTT CTTTGTGTTCT	60
GATTATTTGG TGTGTGTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTGTT	120
CTCTCCATCC TCGGGCATTC TTCCCCAAATT TATATACCAAG TCTTCGTCCA TCCACACGCT	180
CCAGAAATTTC TCTTTTGAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGGTATGCT	240
TGCTGTTGTT CTTCTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA	300
AGACGCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC TCCTTTCA TATCAGGTGA CTCTGCAAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCGGC AGAAAGTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAATAGT TCTNGTCTT CCAGGTGTT ATGATGGAAG	600
GCTCAGTTG TTCAGTCTG ACAATGACAT TGTGTGTTGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCGC GCCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACTCATGC TGCAAAGGTG CTCGCCGTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGT CAGGAGGTGA TGGAGCCACT	840
CCACACCTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG	180
TGAACGTGTC GGTGGTGCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT	234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA	60
ATTTGATAGC AATATTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGITAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA	180
TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAAT TAATTTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC	420
TGGTCTCTAA TCTGCCTTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGA GGTTCAAGAC	120

GCTTCACTGC TTGAAACCTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAAG GGGACAAAGG CTAATCCCAA	240
AACATCAAAG AAAGGAAGGT GGCCTACAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CCTCTGTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTAAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATT ACAGCTATG GGACCTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

## (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAAATTGAA AATTTTATAAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT AATTACAGCT CAAAGCAACT	120
TGGT	124

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC	60
ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCTAGGAA GTCTAGGGAA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAA GTGACACCCT CAGGGGAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAG GTCAGAAAGG GGACTCAGGG CTTCCACCA AGCCCTGCC CACTTGGCCA	180
CCTCCCTTT GGGACCAGCA ATGT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 491 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAA CATTATCTT ATAACAAAAA TTGATAGTT TTAAAGGTTA GTATTGTGA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTTAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTGTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTCTT GTATCAATT CTTTGTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCAAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420

CAATTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT	480
ATCACTCTTG T	491

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 484 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTGAAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC	300
AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTG CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTTC	480
CANT	484

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAACACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTGTTTG T	151

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC	120
AAGGGACAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTTATCCT TTAAAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA	120
ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAACTAGTT	180
TTGACTTCTA AGTTTGTT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAGTTA TCAGAAACTC ACTCAATTTT	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGGCAC	120
TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 154 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT  
 GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC       60  
 TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT   120  
    154

## (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA   30

## (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAGTCATT TCAGCACCCCT TTGCTCTTCA AACTGACCA TCTTTTATAT TTAATGCTTC  
 CTGTATGAAT AAAATGGTT ATGTCAAGT   60  
    89

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGCTTGTG GCTNTCCAA ACCGCACACC	120
CCAACCTCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCCAN GAGGAATCAT GCCTGGCGA TGCAANGGTG CCAACAGGAG	360
GGGGCGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG	60
--	----

AGAACCCGTG TGCCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG	120
AGGAACTAAC TGCACCCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT	180
TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT	240
TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC	300
TGTTT	305

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 385 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA CTCCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTTA GGAATGCTGA	60
GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC	120
CCCTTTTAAA AAAGGGGACT TGCTAAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC	180
TGTGCTGTGC TGGAGATTCA CTTTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG	240
CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG	300
CCTCTCCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC	360
CATAGTTTCT GTGCTAGTGG ACCGT	385

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA	60
GTTTTTTTAA TGG	73

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 536 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGGCTC	TCACCCTCCT	CTCCTGCAGC	60
TCCAGCTTTG	TGCTCTGCCT	CTGAGGAGAC	CATGGCCCAG	CATCTGAGTA	CCCTGCTGCT	120
CCTGCTGCC	ACCCTAGCTG	TGGCCCTGGC	CTGGAGCCCC	AAGGAGGAGG	ATAGGATAAT	180
CCCGGGTGGC	ATCTATAACG	CAGACCTCAA	TGATGAGTGG	GTACAGCGTG	CCCTTCACTT	240
CGCCATCAGC	GAGTATAACA	AGGCCACCAA	AGATGACTAC	TACAGACGTC	CGCTGCGGGT	300
ACTAAGAGCC	AGGCAACAGA	CCGTTGGGGG	GGTGAATTAC	TTCTTCGACG	TAGAGGTGGG	360
CCGAACCATA	TGTACCAAGT	CCCAGCCAA	CTTGGACACC	TGTGCCTTCC	ATGAACAGCC	420
AGAACTGCAG	AAGAACAGT	TGTGCTCTTT	CGAGATCTAC	GAAGTTCCCT	GGGGAGAACA	480
GAANGTCCCT	GGGTGAAATC	CAGGTGTCAA	GAAATCCTAN	GGATCTGTTG	CCAGGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA	ACAGGGGCC	TCTCAGCCCT	CCTAATGACC	TCCGGCCTAG	CCATGTGATT	60
TCACTTCCAC	TCCATAACGC	TCCTCATACT	AGGCCTACTA	ACCAACACAC	TAACCATATA	120
CCAATGATGG	CGCGATGTAA	CACGAGAAAG	CACATACCAA	GGCCACCA	CACCACCTGT	180
CCAAAAAGGC	CTTCGATACG	GGATAATCCT	ATTATTATTACC	TCAGAAGTTT	TTTCTTCGC	240
AGGGATTTT	CTGAGCCTTT	TACCACTCCA	GCCTAGCCCC	TACCCCCCAA	CTAGGAGGGC	300
ACTGCCCCC	AACAGGCATC	ACCCCGCTAA	ATCCCCCTAGA	AGTCCCACTC	CTAAACACAT	360
CCGTATTACT	CGCATCAGGA	GTATCAATCA	CCTGAGCTCA	CCATAGTCTA	ATAGAAAACA	420
ACCGAAACCA	AATTATTCAA	AGCACTGCTT	ATTACAATT	TACTGGGTCT	CTATTTT	477

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG	GTACAGTGTG	ATCTCAGCTT	TGCAAACACA	TTTCACAT	AGATAGTACT	60
AGGTATTAAT	AGATATGAA	AGAAAGAAAT	CACACCATT	ATAATGGTAA	GATTGGTTA	120
TGTGATTTA	GTGGTATTT	TGGCACCCCTT	ATATATGTTT	TCCAACTTT	CAGCAGTGAT	180
ATTATTTCCA	TAACCTAAAA	AGTGAGTTG	AAAAAGAAA	TCTCCAGCAA	GCATCTCATT	240
TAATAAAAGG	TTTGTCACT	TTAAAATAC	AGCAATATGT	GACTTTTAA	AAAAGCTGTC	300
AAATAGGTGT	GACCCTACTA	ATAATTATTA	GAAATACATT	AAAAAACATC	GAGTACCTCA	360
AGTCAGTTG	CCTTGAAAAA	TATCAAATAT	AACTCTTAGA	GAAATGTACA	AAAAGAAATG	420
CTTCGTAATT	TTGGAGTANG	AGGTTCCCTC	CTCAATTG	TATTTTAA	AA GTACATGG	480
TAAAAAAAAAA	AATTCAAC	AGTATATAAG	GCTGTAAAAT	GAAGAATTCT	GCC	533

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 511 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	TAAGAACAC	AAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGGTTGAAA	ACCGTTCTNC	AATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAA	GATGGCCTCC	TTGTGCCCTCC	GTCTGTTATG	420
ATTCTCTCC	ATTGCAGCNA	NAAACCCGTT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTGAAG	NACCNGGAGG	A			511

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 499 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	GTTAACCTTG	CCAGTCTTTC	TCTTCAAGCC	AGGGTGCATC	240

CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAAGTTGACA	300
CTCTGCATTA AATCTATTG CCATTCTGA AAAAAAAA AAAAAAAGGG CGGCCGCTCG	360
ANTCTAGAGG GCCCGTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGCCAGC	420
CATCTGTTGT TTGCCCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCACT	480
GTCCTTCCT AANTAAAAT	499

## (2) INFORMATION FOR SEQ ID NO:74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTG GGATTCAAGCC GCGAAGAGAT	60
TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT	120
TCCAGGCCCA CGGCTCAAGT GAATTGAAAT ACTGCATTAA CAGTGTAGAG TAACACATAA	180
CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA	240
AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG	300
GGCTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC	360
CAGTTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTG AATGGGTTCT	420
ACTGAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTATTTA CACTCTTGAT	480
TCTACAATGT AGAAAATGAA GGAAATGCC CAAATTGTAT GGTGATAAAA GTCCCGT	537

## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC	60
TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTGTT GCCATCATCA	120
CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG	180
TGGCACAGG AGGCCATCTT TTCCTCATCG GTTATTGTCC CTAGAACGCGT CTTCTGAGGA	240
TCTAGTTGGG CTTCTTTCT GGGTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA	300
TCATTATTGT ATAACGGTTT TCAAACCNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA	360
CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC	420
CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACAA TCCCTGN	467

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTCGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAAA	GATTCAAGGTT	TACTCACGTC	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTCTC	TGAATTGCTA	TGTGTCTGGG	TTTCATCCAT	180
CCGACATTGA	AGTTGACTTA	CTGAAGAACATG	GAGAGAGAAAT	TGAAAAGTG	GAGCATTCAAG	240
ACTTGTCTTT	CAGCAAGGAC	TGGTCTTTCT	ATCTCTTGTA	CTACACTGAA	TTCACCCCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360
TTNAGTGGGA	TCGANACATG	TAAGCAGCAN	CATGGGAGGT			400

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC	TTGGTGTTC	AAGCCCTGC	AGGAAGCAGA	ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC	CGGCGGGGG	TGCGAGGCTC	GGAGCACCC	TGCCCCTG	TGATTGCTGC	120
CAGGCACTGT	TCATCTCAGC	TTTCTGTCC	CTTGCTCCC	GGCAAGCGCT	TCTGCTGAAA	180
GTTCATATCT	GGAGCCTGAT	GTCTAACGA	ATAAAGGTCC	CATGCTCCAC	CCGAAAAAAA	240
AAAAAAA						248

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTGC CGCTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT	180
GATTAAAAAA AAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCTTTGTT AGGTTTTGGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTCCCT ATTCTTTATT	120
CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG	180
TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTCCTTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTTGGAA GCCAAATTGA	360
TAATATTCTA TGTCTAAAAA GTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTTA	420
TTCCCAGGAA TATGGGTTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTGTT TAATACGTTA ATATGCTTN AATNAACAAG GCNTGACTTA TTTCCAAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTT GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTAA	180
GCAATTCAAG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCAAC	300

TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTT AATTTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAA AAAAAA	476

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCCA TTCCCAGCCT	120
CTCATCCCCA TCTTGACTT TTGCTAGGGT TGGAGGGCGCT TTCCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT	232

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA CAAGTGAGAT TTTAGATATT	240
GTTAACCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAA AAA	383

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG	300
AGCCCTGATG CCTTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTTT	420
TTTCNCATAT TTTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG	120
GAGGACATGG AC GTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCTC CTGGGGCCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA	120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG	180
TGTGAAAGGA TCTCCAGAAG GAGTGCCTGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA	240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCAACCAGCC	300
CTATCATGCC NTTGAACGTG CCGAAGAACCA CCGAGCCTTG TGTGGGGGT GNAGTCTCAC	360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACCTCGC CCAGGNNGAA	420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCT TGTTGGNNNC GCNTNCCTTT	480
T	481

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCGCTG AGAATTCAATT	60
ACTTGGAAAA GCAACTTNAAC GCCTGGACAC TGGTATTAAA ATTCAACATA TGCAACACTT	120
TAAACAGTGT GTCAATCTGC TCCCCTTAATT TGTCAATCACC AGTCTGGAA TAAGGGTATG	180
CCCTATTACAC ACCTGTTAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTTG	240
CACAAGTCCG AAAAAGCAA AAGTAAACAG TTNTTAATT TTAGCCAAT TCACTTCTT	300
CATGGGACAG AGCCATTGTA TTAAAGAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG	360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTT CATATTGGGA	420
TGTTNACNAAGTTATGCT CTTACAGATG GGATGCTTT GTGGCAATTCTG	472

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAACCAGT ATCTCTNAAC ACAACCTCTC ATACCTTGTG GACCTAATT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATTTTTT TACTTTGTA AAAGCTTATG	120
CCTCTTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCCTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAG TCTAGTTNGT	240
TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCNAAC CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA	360

ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTT TTT 413

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 448 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT	CCTCTCTATC	TAGCTCCAGC	CTCTCGCTG	CCCCACTCCC	CGCGTCCCGC	60
GTCCTAGCCN	ACCATGGCCG	GGCCCCCTGCG	CGCCCCGCTG	CTCCTGCTGG	CCATCCTGGC	120
CGTGGCCCTG	GCCGTGAGCC	CCGC GGCCGG	CTCCAGTCCC	GGCAAGCCGC	CGGCCCTGGT	180
GGGAGGCCCA	TGGACCCCGC	GTGGAGAGAAG	AAGGTGTGCG	GCGTGCAGTG	GACTTTGCCG	240
TCGGCNANTA	CAACAAACCC	GCAACNACTT	TTACCNAGCN	CGCGCTGCAG	GTTGTGCCGC	300
CCCAANAAA	TTGTTACTNG	GGGTAANTAA	TTCTTGGAAAG	TTGAACCTGG	GCCAAACNNNG	360
TTTACCAAGAA	CCNAGCCAAT	TNGAACAAATT	NCCCCTCCAT	AACAGCCCCT	TTTAAAAAAGG	420
GAANCANTCC	TGNTCTTTTC	CAAATTTT				448

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG	CACTGGCAC	TGTGATGGAA	CCATTGGGCC	AGGATGCTTT	GAGTTTATCA	60
GTAGTGATTC	TGCCAAAGTT	GGTGTGTAA	CATGAGTATG	TAAAATGTCA	AAAAAATTAGC	120
AGAGGTCTAG	GTCTGCATAT	CAGCAGACAG	TTTGTCCGTG	TATTTGTAG	CCTTGAAGTT	180
CTCAGTGACA	AGTTNNNTCT	GATGCGAAGT	TCTNATTCCA	GTGTTTAGT	CCTTGCATC	240
TTTNATGTTN	AGACTTGCT	CTNTNAAATT	GCTTTGTNT	TCTGCAGGTA	CTATCTGTGG	300
TTTAACAAAA	TAGAANNACT	TCTCTGCTTN	GAANATTGTA	ATATCTTACA	TCTNAAAATN	360
AATTCTCTCC	CCATANNAAA	ACCCANGCCC	TTGGGANAAT	TTGAAAAANG	GNTCCTTCNN	420
AATTCCNNANA	ANNTCAGNTN	TCATAACAACA	NAACNGGANC	CCC		463

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA GGTCTNTNT	ACTGTCGGAC TGTTCANCCA	CCAACTCTAC AAGTTGCTGT	60
CTTCCACTCA CTGTCTGTAA	GCNTNTAAC CCAGACTGTA	TCTTCATAAA TAGAACAAAT	120
TCTTCACCAG TCACATCTTC	TAGGACCTT TTGGATTCAAG	TTAGTATAAG CTCTTCCACT	180
TCCCTTGTTA AGACTTCATC	TGGTAAAGTC TTAAGTTTG	TAGAAAGGAA TTTAATTGCT	240
CGTTCTCTAA CAATGTCCCT	TCCTTGAAGT ATTTGGCTGA	ACAACCCACC TNAAGTCCCT	300
TTGTGCATCC ATTTAAATA	TACTTAATAG GGCATGGTN	CACTAGGTTA AATTCTGCAA	360
GAGTCATCTG TCTGCAAAAG	TTGCGTTAGT ATATCTGCCA		400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT CCAATAATCT TTGTCTGAGG	GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT	AGNTATATAA GGTCACTCCC TGAGTCAGAC	120
ATGCTCTTT GACTACCGTG TGCCAGTGCT	GGTGATTCTC ACACACCTCC NNCCGCTCTT	180
TGTGGAAAAA CTGGCACTTG NCTGGAACTA	GCAAGACATC ACTTACAAAT TCACCCACGA	240
GACACTTGAA AGGTGTAACA AAGCGACTCT	TGCATTGCTT TTTGTCCCTC CGGCACCAGT	300
TGTCAATACT AACCCGCTGG TTTGCCTCCA	TCACATTTGT GATCTGTAGC TCTGGATACA	360
TCTCCTGACA GTACTGAAGA ACTTCTTCTT	TTGTTTCAAA AGCAACTCTT GGTGCCTGTT	420
NGATCAGGTT CCCATTTCCC AGTCCGAATG	TTCACATGGC ATATNTTACT TCCCACAAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGCGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCCTT	120
CCCACGCAGG	CAGCAGCGGG	GCCGGTCAAT	GAACTCCACT	CGTGGCTTGG	GGTTGACGGT	180
TAANTGCAGG	AAGAGGCTGA	CCACCTCGCG	GTCCACCAGG	ATGCCCGACT	GTGCCGGGACC	240
TGCAGCGAAA	CTCCTCGATG	GTCATGAGCG	GGAAGCGAAT	GANGCCCAGG	GCCTTGCCCA	300
GAACCTTCCG	CCTGTTCTCT	GGCGTCACCT	GCAGCTGCTG	CCGCTNACAC	TCGGCCTCGG	360
ACCAGCGGAC	AAACGGCGTT	GAACAGCCGC	ACCTCACCGA	TGCCCANTGT	GTCCGCGCTCC	420
AGGAACGGCN	CCAGCGTGTG	CAGGTCAATG	TCGGTGAANC	CTCCGGGGT	AATGGCG	477

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG	ACCTTGCCCTC	GCATTGTGCT	GCTGGCAGGA	ATACCTTGGC	AAGCAGCTCC	60
AGTCGGAGCA	GCCCCAGACC	GCTGCCGCC	GAAGCTAACG	CTGCCTCTGG	CCTTCCCCCTC	120
CGCCTCAATG	CAGAACCCANT	AGTGGGAGCA	CTGTGTTAG	AGTTAAGAGT	GAACACTGTN	180
TGATTTTACT	TGGGAATTTC	CTCTGTTATA	TAGCTTTCC	CAATGCTAAT	TTCCAAACAA	240
CAACAAACAA	ATAACATGTT	TGCCTGTTNA	GTGTGATAAAA	AGTANGTGAT	TCTGTATNTA	300
AAGAAAATAT	TACTGTTACA	TATACTGCTT	GCAANTTCTG	TATTTATTGG	TNCTCTGGAA	360
ATAAAATATAT	TATTAA					377

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTGAGG	GGTTAGGGTC	CAGTTCCAG	TGGAAGAAC	AGGCCAGGAG	AANTGCGTGC	60
CGAGCTGANG	CAGATTTCCC	ACAGTGACCC	CAGAGCCCTG	GGCTATAGTC	TCTGACCCCT	120
CCAAGGAAAG	ACCACCTTCT	GGGGACATGG	GCTGGAGGGC	AGGACCTAGA	GGCACCAAGG	180
GAAGGCCCA	TTCCGGGGCT	GTTCCCGAG	GAGGAAGGGA	AGGGGCTCTG	TGTGCCCCCC	240
ACGAGGAANA	GGCCCTGANT	CCTGGGATCA	NACACCCCTT	CACGTGTATC	CCACACACAAA	300

TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACTGGCCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA	480
AAAAAAAANA AAAAAA	495

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 472 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG TTTCATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTC TGCTC	60
CCTCTGGAAAG CCTTGCGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATT	120
TAGCTGTTT GAGTTGATTC GCACCACTGC ACCACAACTC AATATGAAAA CTATTTNACT	180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTGT TCATACTGTA TTTATCAAGT	240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA	300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCCTTT GTAAC TTCAC	360
TTGGTTATTT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA	420
TTTANTTCAN TAATTCTTT CCTTGTAC GTTAATTG AAAAGAATGC AT	472

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT TCTTCAAAC TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT	60
GTGGTGAAT TTCAAAATTA TATGTAACCTT CTACTAGTTT TACTTTCTCC CCCAAGTCTT	120
TTTTAACTCA TGATTTTAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT	180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAGTGTCTT GNCGANAATG TTCTAGNTAT	240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGACT NAACCAAAT	300
TGTGTTAGTC TCAATTCTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT	360
GCAGGGTACTC CTCCAGAAA ACNGACAGGG CAGGCTTGCA TGAAAAGTN ACATCTGCGT	420
TACAAAGTCT ATCTTCCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT	476

## (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 479 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTCATA	ATGCTGATAT	GATCTTGAGT	ATAAGAACATGC	ATATGTCAC	AGAACATGGATA	60
AAATAATGCT	GCAAACTTAA	TGTTCTTATG	CAAAATGGAA	CGCTAATGAA	ACACAGCTTA	120
CAATCGAAA	TCAAAACTCA	CAAGTGCCTCA	TCTGTTGTAG	ATTTAGTGTAA	ATAAGACTTA	180
GATTGTGCTC	CTTCGGATAT	GATTGTTCT	CANATCTTGG	GCAATNTTCC	TTAGTCAAAT	240
CAGGCTACTA	GAATTCTGTT	ATTGGATATN	TGAGAGCATG	AAATTTTAA	NAATACACTT	300
GTGATTATNA	AATTAATCAC	AAATTCACT	TATACTGCT	ATCAGCAGCT	AGAAAAACAT	360
NTNNNTTTTA	NATCAAAGTA	TTTGTGTTT	GGAANTGTNN	AAATGAAATC	TGAATGTGGG	420
TTCNATCTTA	TTTTTCCCN	GACNACTANT	TNCCTTTTA	GGGNCTATTTC	TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCTG	CAAATCTATT	CCTACTTGTAA	CGGACTTTGA	180
AGTGATTCA	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCACT	CTGAACACGC	TGGTTATCTA	GATGAGAACAA	GAGAAATAAA	GTCAGAAAAT	300
TTACCTGGAG	AAAAGAGGCT	TTGGCTGGGG	ACCATCCCCT	TGAACCTTCT	CTTAAGGACT	360
TTAAGAAAAA	CTACCACATG	TTGTGTATCC	TGGTGCCGGC	CGTTTATGAA	CTGACCACCC	420
TTTCCAATAA	TCTTGACGCT	CCTGAACCTG	CTCCTCTGCG	A		461

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTCCCC AGCGTCCCT	60
CGCGCCTCT CGGGGCCGA GGAGGAGCGG CTGGCGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGTAC C	171

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TCGGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGCG GCGACAGTCG CAGGTGCAGC GCGGGCCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGA	180
CAGCCGGAAC AGAGCCCGGT GAAGCGGGAG GCCTCGGGGA GCCCCTCGGG AAGGGCGGCC	240
CGAGAGATAC GCAGGTGCAG GTGGCCGCC	269

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT TTTTGGAAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCAAG GTCAACTTCC TTTGTCGTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAACGAAGCA AATAACATGG	180
AGTGGGTGCA CCCTCCCTGT AGAACCTGGT TACAAAGCTT GGGGCAGTTC ACCTGGTCTG	240
TGACCGTCAT TTTCTTGACA TCAATGTTAT TAGAAGTCAG GATATCTTT AGAGAGTCCA	300
CTGTTCTGGA GGGAGATTAG GGTTCTTGCA CAAATCCAAC AAAATCCACT GAAAAAGTTG	360
GATGATCAGT ACGAATACCG AGGCATAITC TCATATCGGT GGCCA	405

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TCAAAATGT	CTACAAATT	AATCCCATT	TACGGTATTT	120
TCAAATCTA	AATTATTCAA	ATTAGCCAAA	TCCTTACCAA	ATAATACCCA	AAAATCAAAA	180
ATATACTTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTAAGGAA	CTAAAATAAA	AAAAAACACT	300
CCGCAAAGGT	TAAAGGGAAC	AACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTC	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAACT	TTTACTCACT	TTGTTTATTT	420
TTTAAACCA	TTGTTGGGC	CCAACACAAT	GGAATCCCCC	CTGGACTAGT		470

(2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT	TTTTTTTTGA	CCCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAA	GGCAGCT	TTT AAAATCAAAC	120
TAAATGGAAA	CTGCCCTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTC	TCTAGCT	TTGACTGTAA	ATTTTGACT	CTTGAAAC	ATCCAAATT	240
ATTTTCTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTTTAT	CTACTATTAG	TAAGTGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATT	CAT ATTCTACCT	420
ACGTTAATAA	AATAGCATTT	TGTGAAGCCA	GCTAAAAGA	AGGCTTAGAT	CCTTTATGT	480
CCATTTAGT	CACTAAACGA	TATCAAAGTG	CCAGAATGCA	AAAGGTTGT	GAACATTT	540
TCAAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTCT	G		581

(2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTTCTCTT CTTTTTTTTT GAAATGAGGA TCGAGTTTTT	60
CACTCTCTAG ATAGGGCATG AAGAAAAC TC ATCTTCCAG CTTTAAAATA ACAATCAAAT	120
CTCTTATGCT ATATCATATT TTAAGTTAAA CTAATGAGTC ACTGGCCTTAT CTTCTCCTGA	180
AGGAAATCTG TTCATTCTTC TCATTATCAT AGTTATATCA AGTACTACCT TGCATATTGA	240
GAGGTTTTTC TTCTCTATTT ACACATATAT TTCCATGTGA ATTTGTATCA AACCTTTATT	300
TTCATGAAA CTAGAAAATA ATGTTTCTTT TGCAATAAGAG AAGAGAACAA TATAGCATTAA	360
CAAAACTGCT CAAATTGTTT GTTAAGTTAT CCATTATAAT TAGTTGGCAG GAGCTAATAC	420
AAATCACATT TACGACAGCA ATAATAAAAC TGAAGTACCA GTTAAATATC CAAAATAATT	480
AAAGGAACAT TTTTAGCCTG GGTATAATTG GCTAATTAC TTTACAAGCA TTTATTAGAA	540
TGAATTACACA TGTTATTATT CCTAGCCCAA CACAATGG	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTTAT TTTTATATTT AAAATTCTATA	60
GAAAAGTGCC TTACATTAA TAAAAGTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT	120
GTCTTGAACA CCAATATTA TTTGAGGAAA ATACACCAAAT ATACATTAAG TAAATTATTT	180
AAGATCATAG AGCTTGTAAG TGAAAAGATA AAATTTGACC TCAGAAACTC TGAGCATTAA	240
AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTG TTTAATTGG TGATGAATAT	300
GGGGTGTCAAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA	360
TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTTCTCAA TCTTTAAGG	420
GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTCTA TGGAAGGATT	480
AGATATGTTT CCTTTGCCAA TATTAAAAAA ATAATAATGT TTACTACTAG TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTTT TTTTTTAGTC AAGTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC	60
ATTTATTAGC TCTGCAACTT ACATATTAA ATTAAAGAAA CGTTTAGAC AACTGTACAA	120
TTTATAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT	180
TCTCCCACCA ACTAATGAAC AGAACATTA GTTAAATTAA ATTAGTAGAT ATACACTGCT	240
GCAAACGCTA ATTCTCTCT CCATCCCCAT GTGATATTGT GTATATGTGT GAGTTGGTAG	300
AATGCATCAC AATCTACAAT CAACAGCAAG ATGAAGCTAG GCTGGCTTT CGGTGAAAAT	360
AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA	420
CCGCTTCCTC AAAGGCGCTG CCACATTGT GGCTCTTGC ACTTGTTC AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA CTGCAGGGCA TCTCGGTCAT GGAGCTGTCC GGCCTGGCCC CGGGCCCCGTT	60
CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGACC GGCCCGGCTC	120
CCGCTACGAC GTGAGCCGCT TGGGCCGGG CAAGCGCTCG CTAGTGCTGG ACCTGAAGCA	180
GCCGCCGGGA GCCGCCGTGC TGCGGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC	240
CTTCCGCCGC GGTGTCATGG AGAAACTCCA GCTGGGCCCA GAGATTCTGC AGCGGGAAAA	300
TCCAAGGCTT ATTTATGCCA GGCTGAGTGG ATTGGCCAG TCAGGAAGCT TCTGCCGGTT	360
AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAAGGTGT CTCTAAAAA TTGGCAGAAG	420
TGGTGAAGAT CCGTATGCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGCCCTTAT	480
GTGTGCACTG GCCATTATAA TGGCTTTTG TGACCGACA CGCACTGACA AGGGTCAGGT	540
CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAATCA	600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT	660
CTATACGACT TACAGGACAG CAGATGGGA ATTCACTGGCT GTTGGAGCAA TAGAACCCCA	720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT	780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTG CAAAGAAGAC	840
GAAGGCAGAG TGGTGTAAA TCTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC	900
TTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCAAGTGA	960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTT AACACCCAG CCATCCCTTC	1020
TTTCAAAAGG GATCCTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAG AATTGGATT	1080
CAGCCCGGAA GAGATTTATC AGCTTAACCTC AGATAAAATC ATTGAAAGTA ATAAGTAA	1140
AGCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTACAGTG	1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCTA	1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGTATGATT GAATTCTAA	1320
AATGGTTATC ATTAGGGCTT TTGATTATA AAACTTTGGG TACTTATACT AAATTATGGT	1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTGTTGAT ATTAAGATTC TTGACTTATA	1440
TTTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATTT	1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT	1560

AAAAGTCACG TGAAACAAAA AAAAAAAA AAAA AAAAAA AAAAAA AAAAAA AAAAAA	1620
A	1621

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10          15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20          25          30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35          40          45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50          55          60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65          70          75          80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85          90          95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100         105         110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115         120         125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130         135         140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys
145         150         155         160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165         170         175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180         185         190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195         200         205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210         215         220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225         230         235         240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245         250         255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260         265         270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275         280         285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val

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290	295	300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu		
305	310	315
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala		
325	330	335
Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu		
340	345	350
Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn		
355	360	365
Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu		
370	375	380

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCTACT	GAGCCAGCGC	CTGGCCTCT	ACCTGCCGA	CAGCTGGAAC	120
CAGTGCACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGGGC	TGGGCTGCCG	GCTGACCCCG	180
GGTTGTACC	ACCTGGGCCG	CACTGCTCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCGG	240
CTGCTTCACA	TCTTCACGGT	CAACAAACAG	CTGGGGCCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCTCTGGCG	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCTT	GAGGCCACGG	GACAGTGA	TCCAAGTAT	CCTGCGCCGC	420
GTCTCTTACCC	GTCCCCTACTT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTCG	GAGCCCGGCT	TCTGGGCACA	CCCTCCTGGG	540
GCCCAGGCCG	GCACCTCGCT	CTCCCAGTAT	GCCAAGTGGC	TGGTGGTGCT	GCTCCTCGTC	600
ATCTTCCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAGTTAC	660
ACATTGGCA	AAGTACAGGG	CAACAGCGAT	CTCTACTTGA	AGGCGCAGCG	TTACCGCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCCGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCCCTGC	TCAGGCAATT	GTGCAGGCGA	CCCCGGAGCC	CCCAGCCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTTCTAAG	GAAGCCGAGC	GGAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAAGGTG	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AACAGCGCCT	GAAAGTGTG	GAGCGGGAGG	TCCAGCAGTG	TAGCCCGC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCCTGC	TGCCCCCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAAGCCC	1200
CCACAGGGGA	TTTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380
GGATCAAGGC	CTGGATCCCG	GGCCGTTATC	CATCTGGAGG	CTGCAGGGTC	CTTGGGGTAA	1440
CAGGGACCAC	AGACCCCTCA	CCACTCACAG	ATTCCCTACACA	CTGGGGAAAT	AAAGCCATT	1500
CAGAGGAAAA	AAAAAAAAAA	AAAA				1524

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGAACCAGC	CTGCACGCGC	TGGCTCCGGG	TGACAGCCGC	GCGCCTCGGC	CAGGATCTGA	60
GTGATGAGAC	GTGTCCCCAC	TGAGGTGCC	CACAGCAGCA	GGTGTGAGC	ATGGGCTGAG	120
AAGCTGGACC	GGCACCAAAG	GGCTGGCAGA	AATGGGCGCC	TGGCTGATTC	CTAGGCAGTT	180
GGCGGCAGCA	AGGAGGAGAG	GCCGAGCTT	CTGGAGCAGA	GCCGAGACGA	AGCAGTTCTG	240
GAGTGCCTGA	ACGGCCCCCT	GAGCCCTACC	CGCCTGGCCC	ACTATGGTCC	AGAGGCTGTG	300
GGTGAGCCGC	CTGCTGCGGC	ACCGGAAAGC	CCAGCTCTTG	CTGGTCAACC	TGCTAACCTT	360
TGGCCTGGAG	GTGTGTTGG	CCGCAGGCAT	CACCTATGTG	CCGCCTCTGC	TGCTGGAAGT	420
GGGGTAGAG	GAGAAGTTCA	TGACCATGGT	GCTGGGCATT	GGTCCAGTGC	TGGGCTGGT	480
CTGTGTCGG	CTCCTAGGCT	CAGCCAGTGA	CCACTGGCGT	GGACGCTATG	GCCGCCGCG	540
GCCCTTCATC	TGGGCACTGT	CCTTGGGCAT	CCTGCTGAGC	CTCTTTCTCA	TCCCAAGGGC	600
CGGCTGGCTA	GCAGGGCTGC	TGTGCCCGGA	TCCCAGGCC	CTGGAGCTGG	CACTGCTCAT	660
CCTGGCGTG	GGGCTGCTGG	ACTTCTGTGG	CCAGGTGTGC	TTCACTCCAC	TGGAGGCCCT	720
GCTCTCTGAC	CTCTTCCGGG	ACCCGGACCA	CTGTCGCCAG	GCCTACTCTG	TCTATGCCCT	780
CATGATCAGT	CTTGGGGGCT	GCCTGGGCTA	CCTCCTGCCT	GCCATTGACT	GGGACACCA	840
TGCCCTGGCC	CCCTACCTGG	GCACCCAGGA	GGAGTGCCTC	TTTGGCTCTGC	TCACCCCTCAT	900
CTTCCTCACC	TGCGTAGCAG	CCACACTGCT	GGTGGCTGAG	GAGGCAGCGC	TGGGCCCCAC	960
CGAGCCAGCA	GAAGGGCTGT	CGGCCCCCTC	CTTGTGCGCC	CACTGCTGTC	CATGCCGGC	1020
CCGCTTGGCT	TTCCGGAACC	TGGGCGCCCT	GCTTCCCCGG	CTGCACCAAGC	TGTGCTGCCG	1080
CATGCCCGC	ACCCCTGCGC	GGCTCTTCGT	GGCTGAGCTG	TGCAGCTGGA	TGGCACTCAT	1140
GACCTTCACG	CTGTTTTACA	CGGATTCCTG	GGGGAGGGGG	CTGTACCAAGG	CGGTGCCCAG	1200
AGCTGAGCCG	GGCACCGAGG	CCCGGAGACA	CTATGATGAA	GGCGTTCGGA	TGGGAGCCT	1260
GGGGCTGTT	CTGCAGTGCG	CCATCTCCCT	GGTCTTCTCT	CTGGTCATGG	ACCGGCTGGT	1320
GCAGCGATTC	GGCACTCGAG	CAGTCTATTT	GGCCAGTGTG	GCAGCTTCC	CTGTGGCTGC	1380
CGGTGCCACA	TGCTGTCCC	ACAGTGTGGC	CGTGGTGACA	GCTTCAGCCG	CCCTCACCGG	1440
GTTCACCTTC	TCAGCCCTGC	AGATCTGCG	CTACACACTG	GCCTCCCTCT	ACCACCGGG	1500
GAAGCAGGTG	TTCCTGCCC	AATACCGAGG	GGACACTGGA	GGTGTAGCA	GTGAGGGACAG	1560
CCTGATGACC	AGCTTCTGCG	CAGGCCCTAA	GCCTGGAGCT	CCCTTCCCTA	ATGGACACGT	1620
GGGTGCTGGA	GGCAGTGGCC	TGCTCCACC	TCCACCCCGC	CTCTGCGGGG	CCTCTGCTG	1680
TGATGTCTCC	GTACGTGTGG	TGGTGGGTGA	GCCCACCGAG	GCCAGGGTGG	TTCCGGGCCG	1740
GGGCATCTGC	CTGGACCTCG	CCATCTGGA	TAGTGCCTTC	CTGCTGTCCC	AGGTGGCCCC	1800
ATCCCTGTT	ATGGGCTCCA	TTGTCAGCT	CAGCCAGTCT	GTCACTGCT	ATATGGTGTG	1860
TGCGCAGGC	CTGGGTCTGG	TCGCCATTTC	CTTTGCTACA	CAGGTAGTAT	TTGACAAGAG	1920
CGACTTGGCC	AAATACTCAG	CGTAGAAAAC	TTCCAGCACA	TTGGGGTGG	GGGCCTGCCT	1980
CACTGGGTCC	CAGCTCCCCG	CTCCTGTTAG	CCCCATGGGG	CTGCCGGGCT	GGCCGCCAGT	2040
TTCTGTTGCT	GGCAAAGTAA	TGTGGCTCTC	TGCTGCCACC	CTGTGCTGCT	GAGGTGCGTA	2100
GCTGCACAGC	TGGGGGCTGG	GGCGTCCCTC	TCCTCTCTCC	CCAGTCTCTA	GGGCTGCCTG	2160
ACTGGAGGCC	TTCCAAGGGG	GTTCAGTCT	GGACTTATAC	AGGGAGGCCA	GAAGGGCTCC	2220
ATGCACTGGA	ATGCGGGGAC	TCTGCAGGTG	GATTACCCAG	GCTCAGGGTT	AACAGCTAGC	2280
CTCCTAGTTG	AGACACACCT	AGAGAAGGGT	TTTTGGGAGC	TGAATAAACT	CAGTCACCTG	2340
GTTCCTCCATC	TCTAACGCCCC	TTAACCTGCA	GCTTCGTTTA	ATGTAGCTCT	TGCATGGGAG	2400
TTTCTAGGAT	AAAACACTCC	TCCATGGGAT	TTGAACATAT	GACTTATTG	TAGGGAAAGA	2460

GTCCTGAGGG	GCAACACACA	AGAACCCAGGT	CCCCTCAGCC	CACAGCACTG	TCTTTTGCT	2520
GATCCACCCC	CCTCTTACCT	TTTATCAGGA	TGTGGCCTGT	TGGTCCTTCT	GTGCCATCA	2580
CAGAGACACA	GGCATTTAAA	TATTTAACTT	ATTATTTAA	CAAAGTAGAA	GGGAATCCAT	2640
TGCTAGCTTT	TCTGTGTTGG	TGTCTAATAT	TTGGGTAGGG	TGGGGGATCC	CCAACAATCA	2700
GGTCCCCCTGA	GATAGCTGGT	CATTGGGCTG	ATCATTGCCA	GAATCTTCTT	CTCCTGGGGT	2760
CTGGCCCCCCC	AAAATGCCA	ACCCAGGACC	TTGGAAATTIC	TAETCATCCC	AAATGATAAT	2820
TCCAAATGCT	GTTACCCAAG	GTTAGGGTGT	TGAAGGAAGG	TAGAGGGTGG	GGCTTCAGGT	2880
CTCAACGGCT	TCCCTAACCA	CCCCTCTTCT	CTTGGGCCAG	CCTGGTTCCC	CCCACTTCCA	2940
CTCCCCTCTA	CTCTCTCTAG	GAETGGGCTG	ATGAAGGCAC	TGCCCAAAAT	TTCCCCTACC	3000
CCCAACTTTC	CCCTACCCCC	AACTTTCCCC	ACCAAGCTCCA	CAACCCCTGTT	TGGAGCTACT	3060
GCAGGACCAG	AAGCACAAG	TGCGGTTTCC	CAAGCCTTG	TCCATCTCAG	CCCCCAGAGT	3120
ATATCTGTGC	TTGGGGAAATC	TCACACAGAA	ACTCAGGAGC	ACCCCTGCC	TGAGCTAAGG	3180
GAGGTCTTAT	CTCTCAGGGG	GGGTTTAAGT	GCCGTTTGCA	ATAATGTCGT	CTTATTATT	3240
TAGCGGGGTG	AATATTTAT	ACTGTAAGTG	AGCAATCAGA	GTATAATGTT	TATGGTGACA	3300
AAATTAAAGG	CTTTCTTATA	TGTTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3360
AAAAAAAAARA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAATAA	AAAAAAAAAA	AAAAAAAAAA	3410

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGGCGT	CCCTCTGCC	GCCCACCTCAG	TGGCAACACC	CGGGAGCTGT	TTTGTCCCTTT	60
GTGGAGCCTC	AGCAGTTCCC	TCTTCAGAA	CTCACTGCCA	AGAGCCTGA	ACAGGAGCCA	120
CCATGCAGTG	CTTCAGCTTC	ATTAAGACCA	TGATGATCCT	CTTCAATTG	CTCATCTTTC	180
TGTGTGGTGC	AGCCCTGTTG	GCAGTGGGCA	TCTGGGTGTC	AATCGATGGG	GCATCCTTTC	240
TGAAGATCTT	CGGGCCACTG	TCGTCAGTG	CCATGCAGTT	TGTCAACGTG	GGCTACTTCC	300
TCATCGCAGC	CGGCCTTGTG	GTCTTTGCTC	TTGGTTTCC	GGGCTGCTAT	GGTGCTAAGA	360
CTGAGAGCAA	GTGTGCCCTC	GTGACGTTCT	TCTTCATCCT	CCTCCTCATC	TTCATGCTG	420
AGGTTGCAGC	TGCTGTGGTC	GCCTTGGTGT	ACACCACAA	GGCTGAGCAC	TTCCGTACGT	480
TGCTGGTAGT	GCCTGCCATC	AAGAAAGATT	ATGGTTCCCA	GGAAGACTTC	ACTCAAGTGT	540
GGAAACACCAC	CATGAAAGGG	CTCAAGTGCT	GTGGCTTCAC	CAACTATACG	GATTTTGAGG	600
ACTCACCCCTA	CTTCAAAGAG	AACAGTGCT	TTCCCCCATT	CTGTTGCAAT	GACAACGTCA	660
CCAACACAGC	CAATGAAACC	TGCACCAAGC	AAAAGGCTCA	CGACCAAAAA	GTAGAGGGTT	720
GCTTCAATCA	GCTTTTGAT	GACATCCGAA	CTAATGCAGT	CACCGGGGT	GGTGTGGCAG	780
CTGGAATTGG	GGGCCTCGAG	CTGGCTGCCA	TGATTGTGTC	CATGTATCTG	TACTGCAATC	840
TACAATAAGT	CCACTTCTGC	CTCTGCCACT	ACTGCTGCCA	CATGGGAAC	GTGAAGAGGC	900
ACCCCTGGCAA	GCAGCAGTGA	TTGGGGGAGG	GGACAGGATC	TAACAATGTC	ACTTGGGCCA	960
GAATGGACCT	GCCCTTTCTG	CTCCAGACTT	GGGGCTAGAT	AGGGACCACT	CCTTTAGCG	1020
ATGCCCTGACT	TTCCCTCCAT	TGGTGGGTGG	ATGGGTGGGG	GGCATTCCAG	AGCCTCTAAG	1080
GTAGCCAGTT	CTGTTGCCA	TTCCCCCAGT	CTATTAAACC	CTTGATATGC	CCCTCTAGGCC	1140
TAGTGGTGAT	CCCAGTGCTC	TACTGGGGGA	TGAGAGAAAG	GCATTTATA	GCCTGGCAT	1200
AAGTGAAATC	AGCAGAGCCT	CTGGGTGGAT	GTGTAGAAGG	CACTTCAAAA	TGCATAAAACC	1260
TGTTACAATG	TTAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1289

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1           5                   10          15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
 20          25                   30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
 35          40                   45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
 50          55                   60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
 65          70                   75          80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
 85          90                   95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
 100         105                  110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
 115         120                  125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
 130         135                  140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
 145         150                  155          160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
 165         170                  175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
 180         185                  190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
 195         200                  205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr

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210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala		
1	5	10
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu		
20	25	30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val		
35	40	45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly		
50	55	60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly		
65	70	75
Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile		
85	90	95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu		
100	105	110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
                   115                  120                  125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
                   130                  135                  140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
                   145                  150                  155                  160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
                   165                  170                  175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
                   180                  185                  190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
                   195                  200                  205  
 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly  
                   210                  215                  220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His  
                   225                  230                  235                  240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
                   245                  250                  255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
                   260                  265                  270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
                   275                  280                  285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
                   290                  295                  300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
                   305                  310                  315                  320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
                   325                  330                  335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
                   340                  345                  350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala  
                   355                  360                  365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
                   370                  375                  380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
                   385                  390                  395                  400

89

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
                  405                        410                        415  
  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
                  420                        425                        430  
  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
                  435                        440                        445  
  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser  
                  450                        455                        460  
  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
                  465                        470                        480  
  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
                  485                        490                        495  
  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
                  500                        505                        510  
  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
                  515                        520                        525  
  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
                  530                        535                        540  
  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
                  545                        550

## (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 241 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
  1                 5                       10                       15  
  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
  20                 25                       30  
  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
  35                 40                       45  
  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly

90

50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu		
225	230	235
Gln		

## (2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCTC TCCCCTCCTC TGAATTAAAT TCTTCAACT TGCAATTGC AAGGATTACA	60
CATTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAA GTGTCTTGTTGT TTAAAAATTAC	120
TTGGTTGTG AATCCATCTT GCTTTTCCC CATTGGAAC AGTCATTAAC CCATCTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATIC TGACAGGTGA ATTGGATGGT	240
TCTCAGAACC ATTTCACCCA GACAGCCTGT TTCTATCCTG TTTAATAAAAT TAGTTGGGT	300
TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTACAT AAAAGTCTGT GACTTGAAAGT	360
TTAGTC	366

## (2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTTCT ATATTATAGC AAAATTAAAA TCTACCCGTA TTCTAATATT	60
GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTTCATAT TTTAAGACAC ATGATTATTC CTATTTAGT AACCTGGTTC	180
ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	282

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTATCCT CCCTCCTGAA ACAATTGCAA ATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

## (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGGA TCTCTGATTG CCGCACAAATC TGAGTGGAAA  
AANTCCTGGG T

60

71

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA  
GAAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC  
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT  
AATGGANTCA AGANACTCCC AGGCCTCAGC GT

60

120

180

212

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC  
CTCCGCCGGC GCAGAACATG CTGGGGTGGT

60

90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AACCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATT CAT GGTTCTTTG GGAATTCC TT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCA CTGTGCCACA GGTCCCTGTT GACAGTGC GG T	171

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA	60
TTATCAANT A TTGTGT	76

(2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTCCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT	60
CAATGTGCTG GGTCATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTAA ATTCTCTTGG	120
TTAACAGATTTG T	131

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GAAAAATTGC GTTACCAACT ATACCACTGG	60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA	120
CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT	180
TTGCCTCACCC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAAGAAAAA AAGACAGTGG	240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC	300
CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG	360
CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC	420
CTCTTGCTT GT	432

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT	60
AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAATTT GT	112

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACACCGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
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## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGTCTCCCCT CTACCAGCTC	60
ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGCG TCTCTGCTCA	120
TTCTCTCTGA AGTCTAGGTT ACCCATTTG GGGACCCATT ATAGGCAATA AACACAGTTC	180
CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT	240
TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT	300
AGGCTGCCTT CTTTCCATG TCC	323

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATA	60
TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCA	120
TAGCACATTG ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAAC CTCTTTGACA	60
TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTCCTCATCG TGTTTGCCG ATCTCTGGC TAATCGTGGT ATCCTCCATG TTATTAGTAA	180
TTCTGTATTG CATTGTTA ACGCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTATTTAAA AGCTCTTATT TTGTTGGTCAT TAAAATGGCA ATTATGTGC AGCACTTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTT GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCAGA TAAAACATT TGAAGAGCTC CAAAATGAGA	120
GTTCTCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCCTCTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGGTACG GATTGTGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTTGCCA	TTTTGTATAT	ATAAACAAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAACTCGAT	TTCAAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTTG	TATCTCGGGT	180
TTTAGCAAGT	TAAAATGAAN	ATGACAGGAA	AGGCTTATTT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAACT	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGGAAGCCT	300
GTAACAATCT	ACAATTGGTC	CA				322

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTAT	CTGCATAATT	60
CTTGTTTTTC	TTTCCATCTG	GCTCCTGGGT	TGACAATTG	TGGAAACAAC	TCTATTGCTA	120
CTATTTAAAA	AAAATCACAA	ATCTTCCCT	TTAAGCTATG	TTNAATTCAA	ACTATTCTG	180
CTATTCCCTGT	TTTGTCAAAG	AAATTATATT	TTTCAAAATA	TGTNTATTTG	TTTGATGGGT	240
CCCACGAAAC	ACTAATAAAA	ACCACAGAGA	CCAGCCTG			278

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GT	TANAAAAA	CTTGT	TTAGC	TCCATAGAGG	AAAGAATGTT	AAAC	TTTGTA	TTT	AAAACA	60			
GATT	CTCTG	AGGT	AAACT	TGG	TTTCAA	ATG	TAT	TTT	TACTGTATT	TTG	C	TTTGG	120
T													121

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTT	ANAACC	ATGC	CCTAGCA	CATC	CAGA	AATC	CCTAAAGAA	CATC	AGTATA	ATC	CCTATA	ACC			
AT	ANCA	AGTG	GTG	ACTGG	TT	AAGCG	TGCGA	CAAAG	GTCA	CTG	GCAC	ATT	ACTGTGTG	60	
AA	ACTT	GATA	CTT	TTG	TCT	AAG	TAGGA	AC	TAGTAT	ACAG	TNC	CTAGG	AN	120	
GG	GTG	CCCC	CA	ACTC	CTGC	AG	CCG	TCT	CTG	GCC	AG	CC	TGNA	AGG	180
CC	AC	CTCA	AT	AA	GG	GC	CCT	CT	GTG	CC	AG	CT	GA	ACTTCG	240
TT	CCC	AA	AGG	AA	GG	GC	CATG	CT	GA	ATT	GG	CTG	AA	AC	300
CC	AA	AGG	GA	AA	GG	GT	C	TC	GA	AA	AC	GT	GAG		350

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGT	ACCGT	GA	AGACGACAGA	AG	TG	CAT	GG	CAG	GAC	AG	GC	AG	GG	CC	GG	TT	60	
G	TG	TG	TAT	CCG	AA	T	TC	CTG	TGA	G	AA	AA	AG	AT	GA	TG	AG	60
C	A	C	CTT	GTG	CTT	T	GT	CG	CCT	T	A	AA	AG	CC	AG	TG	GT	120
G	AG	AC	TT	TG	TG	T	CT	GC	CT	G	A	AA	GG	CC	AG	CT	GT	180
A	CT	GT	GT	GT	CT	T	CC	T	CC	T	T	TT	GG	GT	CT	GA	TC	240
A	AA	CT	GC	AG	CC	T	CA	CA	GG	TG	T	TT	GG	GT	GT	GA	CA	300
A	AA	AG	GG	CC	CC	A	CA	CA	GG	T	A	TT	GG	GT	GT	GA	CC	360
C	CC	AG	GG	CC	CC	A	CA	CA	GG	G	T	TT	GG	GT	GT	GA	AC	399
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	CC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
T	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
C	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
G	CC	AG	GA	AC	CC	A	CC	CC	CA	G	A	TT	GG	GT	GT	GA	AC	
A	CC	AG	GA	AC	CC													

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTTAGA NGTTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACCTCTC CAGTAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA	120
TGCTGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTTGCCAC TGTACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTTT TTTTTTTTG TAAAATTC	338

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGCGA TCTGGTTGCG CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTG CAGCCAGCCT AGTGCCCGAA GTGAAGGGAGA	120
ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180

100

ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTAATAAT	300
GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
GCCTGGAAC TGTAAAGT GT	382

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAAANCTT CTTTCTGTTG TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTAAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG	120
TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTAA	180
ATATTTCAGCA TAAAGGAGAA	200

## (2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG	240
TTTTTCTACC AGTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

## (2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 459 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCGAGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAACAGA CGTGTATTTA	60
GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAAACATC ATAGCCAATG ATGCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCACT AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	420
CAGCANGGGT GGGAGGAACC AGCTAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACTTTG TATTGTAAT GGCAAACATC CAGNAGCAAT TCCTAACAA	60
ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGT ATAAACTTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

## (2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC ATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTTC GTTTCTTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

## (2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 173 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCAC TTATCTCATCG AATTTTTAAC CCAAACATCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AACACATTC CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCCTGCTC TCTAACCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

## (2) INFORMATION FOR SEQ ID NO:149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GTGGGGGCCT	120
GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGGTGTGG TATGGGCACA GTGAAGAAC	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGAG T	111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCGAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCAATGGCC TCCAAACATG AAAGTGTCAAG	60
CTTCTGCTCT TATGTCTCTCA TCTGACAACCT CTTTACCATTT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAAGCCGG TTACACAGCT AACTCCCCT GGCCTTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCCTT TGGGAACGT AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240
GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGT AGGCATGCTG	300
GCCCTGGT	308

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 295 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCCT CATTCTATGT	180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

## (2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGTA TATCTGTCCC	120
CTTAGT	126

## (2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCAGCTCT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT	120
GCCTGGTAA TTCACCATT ATTTCCTCCC CCAAACCTCTC TGAGTCTTCC CTAAATATTT	180
CTGGTGGTTC TGACCAAAGC AGGTCACTGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCCCTGT TTTCCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAAGCTGGA	360
NACAGACGGG CTCTTTCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTCCT CTGATGTCCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTT	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACAGGCCAAG GTTGTGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGGCGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC	240
TGCTGTGGTG CGGGGANGTG AANGTGTGTG GTCACATTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGTG GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCACTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTGN	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCA	480
AAGGGAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCA GATGCCTCTC	240
CCACCCCTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTC TAACATCCTG	300
GAGAAAATG GCAGTTTGAC CGAACCTGTT ACAACGGTA GAGGCTGATT TCTAACGAAA	360
CTTGTAGAAT GAAGCCTGGA	380

## (2) INFORMATION FOR SEQ ID NO:161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA	60
GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACGT	177

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA	60
TGCAATGCAT CATGCTATTCT CATACTTAAT GAGGGAGTTG CAGGAGATTG AACCAAGGAAA	120
TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACGTG	180
GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG	240
GGTTATGACA AAGACAACGT CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG	300
GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT	360
TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCTCT AATAGTCAAT	420
GATTGTGTAG CCATGCCTAT CAGTAAAAG ATNTTTGAGC AAACACTTT	469

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG	60
ATCCGCTGTC ATCCACTATT CCTTGCGTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC	120
TGCAGGCCGC CCGCCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT	180
TCCTCTGAGA TGAGT	195

## (2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT AGTGTGGCAC ATCAGGGGCG CATCAGGGTC ACAGTCACTC ATAGCCTCGC	60
CGAGGTCGGA GTCCACACCA CCGGTGTAAG TGTGCTCAAT CTTGGGCTTG GCGCCCACCT	120
TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAACCTCG CCAAAGAATT	180
TTTGCAAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCCTTC AGCTCCTCCT TCGTCAGGTG	240
GATGCCAACC TCGTCTANGG TCCGTGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC	300
GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT	360
NGGGGCCTTT TTGGTGAAC TTC	383

## (2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

## (2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAAGT TTTCTAGAAC	60
TGGAAGGATT GTANTCATCC	120
TGAAAATGGG TTTACTTC	180
AATCCCTCAN CCTTGTTCTT CACNACTGTC	240
TATACTGANA GTGTCA	273
GTC GACACCT GAGCCTGNAT	
TTTCACTCAT CCCTGAGAAG	
CCCTTTCCAG TAGGGTGGC	
AATTCCCAC ACAGCTTCCC AGGCTTCTC	
CCCTGGAAAA CTCCAGCTT	
AGTCCCAGAT ACAC	
ACTCATGG GCTGCCCTGG GCA	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA	60
CTCCACAGTC TCAGTGCAGA AAGATCATCT	120
TCCAGCAGTC AGCTCAGACC AGGGTCAAAG	180
GATGTGACAT CAACAGTTTC TGTTTCAGA ACAGGTTCTA	240
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG	300
GTAAGTTTG CACAGGTGAG	360
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC	420
TCTGTATACT CCACACTGAC	480
CTTGGCCATGG GCAAAGGCC CTACCAACAA AACAAATAGGA	
TCACTGCTGG GCACCAGCTC	
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA	
ACTTTCATAC ATCCAAC	
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC	
TTCTGGGGC CATCAGCTGC	
TCGAACACTG A	

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA	60
AGGGAGTTCA GAGGTGGAGC	120
TCAAGGAGCT CTGCAGGCAT TTTGCAANC CTCTCCANAG	180
CANAGGGAGC AACCTACACT	240
CCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG	266
AGTTGGGTG GGCATTGAT	
GTACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA	
GACGAANATG ANATTGGCCT	
TCAAAGCTAG GGGTCTGGCA GGTGGA	

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1248 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: cDNA
  - vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - x) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACCGG CGAGGACTGC AGCCCCGACT CGCAGCCCTG GCAGGGCGCA 60  
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCCTCTGG TGCATCCGCA GTGGGTGCTG 120  
TCAGCCGCAC ACTGTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG 180  
CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGAGGCCAG CCTCTCCGTA 240  
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC 300  
GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC 360  
GCGGGGAACCT TTTGCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC 420  
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC 480  
CCGCTGTACC ACCCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC 540  
AACGGTGACT CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAAGGGCCT TGTGTCTTTC 600  
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAAACCT CTGCAAATTC 660  
ACTGAGTGGA TAGAGAAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA 720  
ATTGACCCCC AAATACATCC TGCGGAAGGA ATTCAAGGAAT ATCTGTTCCC AGCCCCCTCCT 780  
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC 840  
CCCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC 900  
CCAGGAGTCC AGCCCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCCCTCCT 960  
CTCAGACCCA GGGGCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGGCC 1020  
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCTCAG CCCCTCNTCC CTCAGACCCA 1080  
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGC CCCTTGTGGC ACGTTGACCC 1140  
AACCTTACCA GTTGGTTTTT CATTTTNGT CCCTTCCCC TAGATCCAGA AATAAAGTTT 1200  
AAGAGAAGNG CAAAAAAAG CAAAAAAAG CAAAAAAAG CAAAAAAAG CAAAAAAAG 1248

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 159 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Homo sapiens
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
					20				25					30	
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
	35						40						45		
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly
	50					55				60					
Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu
	65				70				75				80		
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe
				85				90					95		
Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser
	100					105					110				
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe
	115					120				125					
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn
	130					135				140					
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser	
	145				150				155						

## (2) INFORMATION FOR SEQ ID NO:173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGCGTCC	TGGTGCATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCCTGCT	CGCTAACGAC	240
CTCATGCTCA	TCAAGTTGGA	CGAATCCGTG	TCCGAGTCTG	ACACCATCCG	GAGCATCAGC	300
ATTGCTTCGC	AGTGCCTAC	CGCGGGAAAC	TCTTGCCCTCG	TTTCTGGCTG	GGGTCTGCTG	360
GCGAACGGTG	AGCTCACGGG	TGTGTCTCTG	CCCTCTCAA	GGAGGTCTCT	TGCCCAGTCG	420
CGGGGGCTGA	CCCAGAGCTC	TGCGTCCAG	GCAGAACGCC	TACCGTCTG	CAGTGCCTGA	480
ACGTGTCGGT	GGTGTCTGAG	GAGGTCTGCA	GTAAGCTCTA	TGACCCGCTG	TACCACCCCA	540
GCATGTTCTG	CGCCGGCGGA	GGGCAAGACC	AGAAGGACTC	CTGCAACGGT	GACTCTGGGG	600
GGCCCGCTGAT	CTGCAACGGG	TACTTGCAGG	GCCTTGTGTC	TTTCGGAAAA	GCCCCGTGTG	660
GCCAAGTTGG	CGTGCCAGGT	GTCTACACCA	ACCTCTGCAA	ATTCACTGAG	TGGATAGAGA	720

AAACCGTCCA	GGCCAGTTAA	CTCTGGGAC	TGGGAACCCA	TGAAATTGAC	CCCCAAATAC	780
ATCCTGCCGA	AGGAATTCA	GAATATCTGT	TCCCAGCCCC	TCCTCCCTCA	GGCCCAGGAG	840
TCCAGGCC	CAGCCCCCTCC	TCCCTCAAAC	CAAGGGTACA	GATCCCCAGC	CCCTCCTCCC	900
TCAGACCCAG	GAGTCCAGAC	CCCCCAGCCC	CTCCTCCCTC	AGACCCAGGA	GTCCAGCCCC	960
TCCTCCNTCA	GACCCAGGAG	TCCAGACCCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGGGTT	1020
GAGGCC	ACCCCTCTC	CTTCAGAGTC	AGAGGTCCAA	GCCCCCAACC	CCTCGTTCCC	1080
CAGACCCAGA	GGTNNAAGGTC	CCAGCCCCCTC	TTCCNTCAGA	CCCAGNGGTC	CAATGCCACC	1140
TAGATTITCC	CTGNACACAG	TGCCCCCTTG	TGGNANGTTG	ACCCAACCTT	ACCAGTTGGT	1200
TTTTCATTTT	TNGTCCCTTT	CCCCTAGATC	CAGAAATAAA	GTTTAAGAGA	NGNGCAAAAA	1260
AAAAAA						1265

## (2) INFORMATION FOR SEQ ID NO:174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAGCCGC	ACACTGTTTC	CAGAAAGTGAG	TGCAGAGCTC	CTACACCAC	GGGCTGGGCC	60
TGCACAGTCT	TGAGGCCGAC	CAAGAGCCAG	GGAGCCAGAT	GGTGGAGGCC	AGCCTCTCCG	120
TACGGCACCC	AGAGTACAAC	AGACCCCTGC	TCGCTAACGA	CCTCATGCTC	ATCAAGTTGG	180
ACGAATCCGT	GTCCGAGTCT	GACACCATCC	GGAGCATCAG	CATTGCTTCG	CAGTGCCCTA	240
CCGGGGGAA	CTCTTGCTC	GTTCCTGGCT	GGGGTCTGCT	GGCGAACGGT	GAGCTCACGG	300
GTGTGTGTCT	GCCCTCTTC	AGGAGGTCTT	CTGCCAGTC	GCGGGGCTG	ACCCAGAGCT	360
CTGCGTCCCA	GGCAGAATGC	CTACCCGTCT	GCAGTGCCTG	AACGTCTCGG	TGGTGTCTGA	420
NGAGGTCTGC	ANTAACGCTCT	ATGACCCGCT	GTACCAACCCC	ANCATGTTCT	GCGCCGGCGG	480
AGGGCAAGAC	CAGAAGGACT	CCTGCAACGT	GAGAGAGGGG	AAAGGGGAGG	GCAGGGGACT	540
CAGGGAAGGG	TGGAGAAGGG	GGAGACAGAG	ACACACAGGG	CCGCATGCCG	AGATGCAGAG	600
ATGGAGAGAC	ACACAGGGAG	ACAGTGACAA	CTAGAGAGAG	AAACTGAGAG	AAACAGAGAA	660
ATAAACACAG	GAATAAAGAG	AAGCAAAGGA	AGAGAGAAAC	AGAAACAGAC	ATGGGGAGGC	720
AGAAACACAC	ACACATAGAA	ATGCAGTTGA	CCTTCCAACA	GCATGGGCC	TGAGGGCGGT	780
GACCTCCACC	CAATAGAAA	TCCTCTTATA	ACTTTTGACT	CCCCAAAAAC	CTGACTAGAA	840
ATAGCCTACT	GTTGACGGGG	AGCCTTACCA	ATAACATAAA	TAGTCGATTT	ATGCATACGT	900
TTTATGCATT	CATGATATAC	CTTTGTTGGA	ATTTTTGAT	ATTTCTAAGC	TACACAGTTC	960
GTCTGTGAAT	TTTTTAAAT	TGTTGCAACT	CTCCTAAAAT	TTTTCTGATG	TGTTTATTGA	1020
AAAAATCCAA	GTATAAGTGG	ACTTGTGCAT	TCAAACCAGG	GTTGTTCAAG	GGTCAACTGT	1080
GTACCCAGAG	GGAAACAGTG	ACACAGATT	ATAGAGGTGA	AACACGAAGA	GAAACAGGAA	1140
AAATCAAGAC	TCTACAAAGA	GGCTGGGAG	GGTGGCTCAT	GCCTGTAATC	CCAGCACTTT	1200
GGGAGGCGAG	GCAGGCAGAT	CACTTGAGGT	AAGGAGTTCA	AGACCAGCCT	GGCCAAAATG	1260
GTGAAATCCT	GTCTGTACTA	AAAATACAAA	AGTTAGCTGG	ATATGGTGGC	AGGCGCCTGT	1320
AATCCCAGCT	ACTTGGGAGG	CTGAGGCAGG	AGAATTGCTT	GAATATGGGA	GGCAGAGGTT	1380
GAAGTGAGTT	GAGATCACAC	CACTATACTC	CAGCTGGGCC	AACAGAGTAA	GACTCTGTCT	1440
AAAAAAAAAA	AAAAAAAAAA					1459

## (2) INFORMATION FOR SEQ ID NO:175:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1167 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGGCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGG	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGCAG	300
TGCCCTACCG	CGGGGAACCTC	TTGCCTCGTN	TCTGGCTGGG	GTCTGCTGGC	GAACGGCAGA	360
ATGCTTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCCTGCA	ACGGTGACTC	TGGGGGCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGCTTTCG	AAAAAGCCCC	GTGTGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATAACATCCT	GCGGAANGAA	TTCAGGAATA	TCTGTTCCCA	720
GCCCCCTCTC	CCTCAGGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCTC	CNTCAGACGC	AGGAGTCCAG	ACCCCCCAGC	900
CCNTCNTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCNTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGCCC	CCTTGTGGCA	1080
NGTTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTTCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10			15			

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
				20					25			30			

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu		
50	55	60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser		
65	70	75
		80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly		
85	90	95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met		
100	105	110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val		
115	120	125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala		
130	135	140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly		
145	150	155
		160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys		
165	170	175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys		
180	185	190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser		
195	200	205

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: cDNA
  
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GCAGCACTCGC AGCCCTGGCA GGCGGCACTG GTCATGGAAA ACGAATTGTT CTGCTCGGGC	60
GTCCTGGTGC ATCCGCAGTG GGTGCTGTCA GCCGCACACT GTTTCCAGAA CTCCTACACC	120
ATCGGGCTGG GCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA GATGGTGGAG	180
GCCAGCCTCT CCGTACGGCA CCCAGAGTAC AACAGACCCCT TGCTCGCTAA CGACCTCATG	240
CTCATCAAGT TGGACGAATC CGTGTCGAG TCTGACACCA TCCGGAGCAT CAGCATTGCT	300
TCGCAGTGCC CTACCGCGGG GAACTCTTGC CTCGTTTCTG GCTGGGGTCT GCTGGCGAAC	360
GATGCTGTGA TTGCCATCCA GTCCCAGACT GTGGGAGGCT GGGAGTGTGA GAAGCTTCC	420
CAACCCTGGC AGGGTTGTAC CATTTCGGCA ACTTCCAGTG CAAGGACGTC CTGCTGCATC	480

CTCACTGGGT GCTCACTACT GCTCACTGCA TCACCCGGAA CACTGTGATC AACTAGCCAG	540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC TGCTCTATTGT	600
ACTAACCATG CCGATGTTA GGTAAATTG GCGTCACTTG GCCTCAACCA TCTTGGTATC	660
CAGTTATCCT CACTGAATTG AGATTCCTG CTCAGTGTC AGCCATTCCC ACATAATTTC	720
TGACCTACAG AGGTGAGGGG TCATATAGCT CTCAGTGTC AGCCATTCCC ACATAATTTC	780
TTCATTTCTC CTGTTGAGGT GAAAGGTGCG CCCTCTGGAG CCTCCAGGG TGGGTGTGCA	840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTAA ATCCCTCATG	900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTTAGT GTATGCTGTC CATTGATGCA	960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG CCTCCCTGGG	1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA CATTAGGTGC	1080
TTAATAAACAA GAAGCTGTGA TGTAAAAAAA AAAAAAAA	1119

## (2) INFORMATION FOR SEQ ID NO:178:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5						10					15

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
							20		25				30		

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
				35				40				45			

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
					50		55				60				

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
				65		70				75			80		

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
					85				90			95			

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
				100				105				110			

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
					115			120			125				

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
				130				135			140				

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145

150

155

160

Pro Gly Thr Leu

## (2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT	60
CCAGCTGCC CCGGCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT	120
GCCAGGCACT GTTCATCTCA GCTTTCTGT CCCTTGCTC CCGGCAAGCG CTTCTGCTGA	180
AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAAA	240
AAAAAAAAAAA	250

## (2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCCAA CACAATGGCT ACCTTTAACAA	60
TCACCCAGAC CCCGCCCTG CCCGTGCCCC ACGCTGCTGC TAACGACAGT ATGATGCTTA	120
CTCTGCTACT CGGAAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC	180
TGATTTAAAAA AAAAAAAAAA AA	202

## (2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT NAGGTTKKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG	60
AATGTTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT	120
TTATTCCTCT TTCTTCTGAA GATTAATGAA GTGAAAATT GAGGTGGATA AATACAAAAA	180
GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA	240
AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC	300
CTACTCTGTT CCTTGGCTAG AAAAAATTAT AACACAGGACT TTGTTAGTTT GGGAAAGCCAA	360
ATTGATAATA TTCTATGTTT TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW	420

TTTTATTCCC AGGAATATGG KGTTCATTT ATGAATATTA CSCRGGATAG AWGTWTGAGT	480
AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTC	540
CAAAAAAAA AAAAAAAA	558

## (2) INFORMATION FOR SEQ ID NO:182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK GRGGATGCTA AGSCCCRGAGA RWTYGTTGAGT TCCAACCCTG GCTTWTTTTC	60
AGAGGGAAA ATGGGGCCTA GAAGTACAG MSCATYTAGY TGTTGCGMTG GCACCCCTGG	120
CSTCACACAG ASTCCCGAGT AGCTGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG	180
TTWGCAATTCTACGTTGCCAC CTCCAACCTTA AACATTCTTC ATATGTGATG TCCTTAGTCA	240
CTAAGGTTAA ACTTTCCCAC CCAGAAAAGG CAACTTAGAT AAAATCTTAG AGTACTTTCA	300
TACTMTCTCA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGTT GATAGGAANT	360
NTCTCTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGG TAGGCATARA	420
AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAAA ARAAAAAAA AAAAAAAA	479

## (2) INFORMATION FOR SEQ ID NO:183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGTG GCAGTGCCAG CACTGGTGCC	60
AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCCAGCA CCAGTGGTGG CTTCACTGCT	120
GGTGCCAGCC TGACCGCCAC TCTCACATTG GGGCTCTTCG CTGGCCTTGG TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC TGGTGCCTGT GGTTCTCCT ACAAGTGAGA TTTTAGATAT	240
TGTTAACCTT GCCAGTCTT CTCTTCAGC CAGGGTGCAT CCTCAGAAC CTACTCAACA	300
CAGCACTCTA GGCAGGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATT	360
GCCATTCAA AAAAAAAA AAAAAA	384

## (2) INFORMATION FOR SEQ ID NO:184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTYYNT CCRGTATKAC CTCAACGAGC	60
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AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCGAT GGGACAACAG ACCTGCTCAG	120
CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAAC ACCATCAAGA	180
AACGCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC	240
TGATGTCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT CTTCGGACTG	300
TGAGCCCTGA TGCCCTTTTG CCAGCCATAC TCTTTGGCAT CCAGTCTCTC GTGGCGATTG	360
ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGAAACAC ATTTGACTTT	420
TTTTTCTCAT ATTTTAAATT ACTACMAGAW TATTWMAGAW WAAATGAWTT GAAAAACTST	480
AAAAAAAAAAA AAAAAAA	496

## (2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGACTTCC	60
CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTCGGG CAGATTCCCC	120
AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCGTCGGAG CCCGGCTTCT	180
GGGCACACCC TCCTGGGGCC CAGGCGGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG	240
TGGTGCCTGCT CCTCGTCATC TTCTGCTCG TGGCCAAACAT CCTGCTGGTC AACTTGCTCA	300
TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGCGATCTC TACTGGGAAG	360
GCGCAGCGTT ACCGCCTCAT CCGG	384

## (2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC CTCCACAAACC TTGATGAGGT CGTCTGCAGT GGCTCTCGC TTCAATACCGC	60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CYTCCTGGCA TCTTGGGGCG GCNTAATATT	120
CCAGGAAACT CTCAATCAAG TCACCGTCGA TGAAACCTGT GGGCTGGTTC TGTCTCCGC	180
TCGGTGTGAA AGGATCTCCC AGAAGGAGTG CTCGATCTTC CCCACACTTT TGATGACTTT	240
ATTGAGTCGA TTCTGCATGT CCAGCAGGAG GTTGTACCAAG CTCTCTGACA GTGAGGTAC	300
CAGCCCTATC ATGCCGTGTA MCGGCCGAA GARCACCGAG CCTTGTGTGG GGGKKGAAGT	360
CTCACCCAGA TTCTGCATTA CCAGAGAGCC GTGGCAAAG ACATTGACAA ACTCGCCCG	420
GTGGAAAAAG AMCAMCTCCT CGARGTGCTN GCCGCTCCTC GTCMGTGGT GGCAGCGCTW	480
TCCTTTGAC ACACAAACAA GTTAAAGGCA TTTTCAGCCC CCAGAAANTT GTCATCATCC	540
AAGATNTCGC ACAGCACTNA TCCAGTTGGG ATTAAAT	577

## (2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTAA	AGCCTGGACA	CTGGTATTAA	AATTACAAT	ATGCAACACT	120
TTAACACAGTG	TGTCAATCTG	CTCCCYYNAC	TTTGTATC	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATT	ACACCTGTTA	AAAGGGCGCT	AAGCATTTT	GATTCAACAT	CTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAA	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTAAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTG	GCGGAAGAGT	AGCCTTCTA	CTTCACCAGA	CACAACCTCCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATT	CCACTTGCAC	AAGAAGGC	TTTCTTCCTC	AGGC	534

## (2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 761 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAACCAGT	ATCTCTNAAA	ACAACCTCTC	ATACCTTGTG	GACCTAATTT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGT	AAAGCTTATG	120
CCTCTTGGT	ATCTATATCT	GTGAAAGTTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTC	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCAGATN	ACAACACTNA	CAAACCTCTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAATWA	CCTGGTGAGA	ARTTGCATAA	360
ACAGAAATWR	GGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWKTT	WTTCCTCC	420
GCAAAAAACA	TGTACNGACT	TCCCGTTGAG	TAATGCCAAG	TTGTTTTTT	TATNATAAAA	480
CTTGCCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCCTAAC	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTTCATTA	AAAATGTTTG	CTAAATACA	CTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTA	GATTTATGT	AGTATNAAGT	AAAAAANTAC	720
GAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

## (2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACCGGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCCTG	CTGCCTTCTC	TGTCTGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180

AAGGCAGGGG CCACCAAGTCC AGGGGTGGGA ATACAGGGGG TGGGANGTGT GCATAAGAAG	240
TGATAGGCAC AGGCCACCCG GTACAGACCC CTCGGCTCCT GACAGGTNGA TTTCGACCAG	300
GTCATTGTGC CCTGCCAGG CACAGCGTAN ATCTGGAAAA GACAGAAATGC TTTCCTTTTC	360
AAATTTGGCT NGTCATNGAA NGGGCANTTT TCCAANTTNG GCTNGGTCTT GGTACNCTTG	420
GTTCGGCCCA GCTCCNCGTC CAAAAANTAT TCACCCNNCT CCNAATTGCT TGCNGGNCCC	480
CC	482

## (2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTTT TTTTAAAACA GTTTTCACA ACAAAATTAA TTAGAAGAAT AGTGGTTTG	60
AAAACACTCG CATCCAGTGA GAACTACCAT ACACCACATT ACAGCTNGGA ATGTNCTCCA	120
AATGTCTGGT CAAATGATAC AATGGAACCA TTCATCTTA CACATGCACG AAAGAACAAAG	180
CGCTTTGAC ATACAATGCA CAAAAAAAAGGGGGGGGG GACCACATGG ATTAAAATTT	240
TAAGTACTCA TCACATACAT TAAGACACAG TTCTAGTCCA GTCNAAAATC AGAACTGCNT	300
TGAAAATTT CATGTATGCA ATCCAACCAA AGAACTTNAT TGGTGATCAT GANTNCTCTA	360
CTACATCNAC CTTGATCATT GCCAGGAACN AAAAGTTNAANACACNCNGT ACAAAAANAA	420
TCTGTAATTN ANTCAACCT CCGTACNGAA AAATNTTNT TATACACTCC C	471

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA AGGTCTGTT TASTGTCGGM CTGTTCAGCC ACCAACTCTA ACAAGTTGCT	60
GTCTTCCACT CACTGTCGT AAGCTTTTA ACCCAGACWG TATCTTCATA AATAGAACAA	120
ATTCTTCACC AGTCACATCT TCTAGGACCT TTTTGGATT AGTTAGTATA AGCTCTTCCA	180
CTTCCTTGT TAAGACTCTA TCTGGTAAAG TCTTAAGTT TGTAGAAAGG AATTYAATTG	240
CTCGTTCTCT AACAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC	300
CTTTGTGCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC	360
AAGAGTCATC TGTCTGCAAA AGTTGCGTTA GTATATCTGC CA	402

## (2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGTCTACCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCYTYTTT	GAYTACCGTG	TGCCAAGTGC	TGGTGATTCT	YAACACACYT	CCATCCCGYT	180
CTTTGTGGA	AAAACGGCA	CTTKTCTGGA	ACTAGCARGA	CATCACTTAC	AAATTCAACCC	240
ACGAGACACT	TGAAAGGTGT	AACAAAGCGA	YTCTTGCATT	GCTTTTGTC	CCTCCGGCAC	300
CAGTTGTCAA	TACTAACCCG	CTGGTTGCC	TCCATCACAT	TTGTGATCTG	TAGCTCTGGA	360
TACATCTCCT	GACAGTACTG	AAGAACTTCT	TCTTTGTTT	CAAAAGCARC	TCTTGGTGCC	420
TGTTGGATCA	GGTCCCAT	TCCCAGTCYG	AATGTTCACA	TGGCATATT	WACTTCCCAC	480
AAAACATTGC	GATTTGAGGC	TCAGCAACAG	CAAATCCTGT	TCCGGCATTG	GCTGCAAGAG	540
CCTCGATGTA	GCCGGCCAGC	GCCAAGGCAG	GCGCCGTGAG	CCCCACCAGC	AGCAGAAGCA	600
G						601

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCCA	NATCCCACCA	CGAAGATGCG	CTTGTGACT	GAGAACCTGA	TGGGGTCACT	60
GGTCCCGCTG	TAGCCCCAGC	GACTCTCCAC	CTGCTGGAAG	CGGTTGATGC	TGCACTCYTT	120
CCCAACGCAG	GCAGMAGCGG	GSCCGGTCAA	TGAACTCCAY	TCGTGGCTTG	GGGTKGACGG	180
TKAAGTGCAG	GAAGAGGCTG	ACCACTCGC	GGTCCACCAG	GATGCCGAC	TGTGCGGGAC	240
CTGCAGCGAA	ACTCCTCGAT	GGTCATGAGC	GGGAAGCGAA	TGAGGCCCAG	GGCCTTGCCC	300
AGAACCTTCC	GCCTGTTCTC	TGGCGTCACC	TGCAGCTGCT	GCCGCTGACA	CTCGGCCTCG	360
GACCAGCGGA	CAAACGGCRT	TGAACAGCCG	CACCTCACGG	ATGCCAGTG	TGTGCGCCTC	420
CAGGAMMGSC	ACCAGCGTGT	CCAGGTCAAT	GTCGGTGAAG	CCCTCCGCGG	GTRATGGCGT	480
CTGCAGTGT	TTTGTGATG	TTCTCCAGGC	ACAGGCTGGC	CAGCTGCGGT	TCATCGAAGA	540
GTCGCGCCTG	CGTGAGCAGC	ATGAAGGCAGT	TGTCGGCTCG	CAGTTCTTCT	TCAGGAACTC	600
CACGCAAT						608

## (2) INFORMATION FOR SEQ ID NO:194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTGCT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGGCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTCCAAAC	240
AACAACAAACA	AAATAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTATT	GKTNCTSTGG	360
AAATAAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

## (2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTTTC	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAAGG	CCCATTCCGG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCCTCTCA	GTCCCCCTTC	STACACCCCTG	AMCGGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNNG	420
GCARCGTGG	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

## (2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATTS	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTTAT	TATCTTGTA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTTGTA	360
TCACTTGGTT	ATTTTATTGT	AAATGARTTA	CAAATTCTT	AATTTAAGAR	AATGGTATGT	420
WATATTATT	TCATTAATT	CTTTCTKGT	TTACGTWAAT	TTTGAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTGG	AAGTAGTTG	ACCCACATCC	CTATGAGTT	540
TTCTTAAAGAT	GTATAAAAGGT	TGTAGCCAT	CNAACTTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGAATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTATAA	ACTAGCAAAN	660
	AAGT					665

## (2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTNTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTTATAA	NATTTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAAT	CCAAACTGAA	240
CAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTTCT	GAACTTAGA	TTTTCTAGAA	AAATATGTAA	TAGTGATCAG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTTCCC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

## (2) INFORMATION FOR SEQ ID NO:198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTTGN	ATTCANTCT	GTANNAANTA	TTTTCATTAT	GTTTTATTANA	AAAATATNAA	60
TGNTNTCCACN	ACAAATCATN	TTACNTNAGT	AAGAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTAGCACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

## (2) INFORMATION FOR SEQ ID NO:199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTTGA	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGTA	CGGACTTTGA	180
AGTGATTCA	TTCCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTNNGG	CTGGGGACCA	TCCCATTGAA	CCTTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGTN	TGTNGTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCTTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

## (2) INFORMATION FOR SEQ ID NO:200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCCCAAG	TGCAACTCCA	GCTGGGGCCG	TGCAGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGCG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCGTGT	CACGTCCCAC	GACCTTGACG	CCGTCGGGA	180
CAGCCGGAAC	AGAGCCCGT	GAANGCGGGA	GGCCTCGGGG	AGCCCCTCGG	GAAGGGCGGC	240
CCGAGAGATA	CGCAGGTGCA	GGTGGCGGCC				270

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTCA	GTCAACTTCC	TTTGTGTTGG	120
TTGATTGGTT	TGTCTTATG	GGGGCGGGGT	GGGCTAGGGG	AAANCGAAC	ANAANTAAACA	180
TGGAGTGGGT	GCACCCTCCC	TGTAGAACCT	GGTTACNAAA	GCTTGGGGCA	GTTCACCTGG	240
TCTGTGACCG	TCATTTTCTT	GACATCAATG	TTATTAGAAG	TCAGGATATC	TTTTAGAGAG	300
TCCACTGTNT	CTGGAGGGAG	ATTAGGGTTT	CTTGCCAANA	TCCAANCAA	ATCCACNTGA	360
AAAAGTTGGA	TGATNCANGT	ACNGAATACC	GANGGCATAN	TTCTCATANT	CGGTGGCCA	419

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TGGCACTTAA	TCCATTTTTA	TTTCAAAATG	TCTACAAANT	TTNAATNCNC	CATTATACNG	120
GTNATTTNC	AAAATCTAAA	NNTTATTCAA	ATNTNAGCCA	AANTCCTTAC	NCAAATNNAA	180
TACNCNCAA	AATCAAAAT	ATACNTNTCT	TTCAAGAAC	TTNGTTACAT	AAATTAAAAA	240
AATATATACG	GCTGGTGT	TCAAAGTACA	ATTATCTTAA	CACTGCAAAC	ATNTTTNNAA	300
GGAACTAAAA	TAAAAAAAAA	CACTNCCGCA	AAGGTTAAAG	GGAACAAACAA	ATTCTNTTTA	360
CAACANCNC	NATTATAAAA	ATCATATCTC	AAATCTTAGG	GGAATATATA	CTTCACACNG	420
GGATCTTAAC	TTTTACTNCA	CTTTGTTTAT	TTTTTANAA	CCATTGTNTT	GGGCCAAACA	480
CAATGGNAAT	NCCNCNCNC	TGGACTAGT				509

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTG A	CCCCCTCTT	ATAAAAACA	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTT	AAAATCAAAC	120
TAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAC	ATCCAAATT	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGGGCTT	TTTCCTAAA	360
AGGGAAAACA	GGAAGAGANA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTCAAAAG	AAGGCTTAGA	TCCCTTTATG	480
TCCATTTCAG	TCACTAAAAG	ATATCNAAG	TGCCAGAATG	CAAAAGGTTT	GTGAACATT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTTAAA	120
AATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AAACTAATGA	GTCACTGGCT	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	240
TGAGAGGTTT	TTCTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTTGACATA	AGAGAAGAGA	360
CATTACAAAA	CTGCTAAAT	TGTTGTTAA	GNTTATCCAT	TATAATTAGT	420
CTAATACAAA	TCACATTAC	NGACNAGCAA	TAATAAAAAC	GAAGTACCA	480
AAAATAATTA	AAGGAACATT	TTTAGCCTGG	GTATAATTAG	CTAATTCACT	540
TTATTNAGAA	TGAATTACACA	TGTTATTATT	CCNTAGCCC	ACACAATGG	589

## (2) INFORMATION FOR SEQ ID NO:205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT TTTTTTCAGT AATAATCAGA ACAATATTAA TTTTTATATT TAAAATTCA	60
AGAAAAGTGC CTTACATTAA ATAAAAGTTT GTTTCTCAA GTGATCAGAG GAATTAGATA	120
TNGTCTTGAA CACCAATATT AATTGAGGA AAATACACCA AAATACATTA AGTAAATTAT	180
TTAACATCAT AGAGCTTGTAA AGTAAAAAGA TAAAATTGA CCTCAGAAAC TCTGAGCATT	240
AAAAATCCAC TATTAGCAAA TAAATTACTA TGGACTTCTT GCTTTAATTG TGTGATGAAT	300
ATGGGGTGTG ACTGGTAAAC CAACACATTC TGAAGGATAC ATTACTTAGT GATAGATTCT	360
TATGTAATTG CTANATNAC GTGGATATGA GTTGACAAGT TTCTCTTTCT TCAATCTTT	420
AAGGGGCNGA NGAAATGAGG AAGAAAAGAA AAGGATTACG CATACTGTTC TTTCTATNGG	480
AAGGATTAGA TATGTTTCCT TTGCCAATAT TAAAAAAATA ATAATGTTTA CTACTAGTGA	540
AACCC	545

## (2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTTT TTTTTTAGTC AAGTTTCTNA TTTTTATTAT AATTAAAGTC TTGGTCATT	60
CATTTATTAG CTCTGCAACT TACATATTAA AATTAAAGAA ACGTNTTAG ACAACTGTNA	120
CAATTATATAA ATGTAAGGTG CCATTATTGA GTANATATAT TCCTCCAAGA GTGGATGTGT	180
CCCTTCTCCC ACCAACTAAT GAANCAGCAA CATTAGTTA ATTTTATTAG TAGATNATAC	240
ACTGCTGCAA ACGCTAATTTC TCTTCTCCAT CCCCCATGTNG ATATTGTGTAT TATGTGTGAG	300
TTGGTNAGAAA TGCATCANCA ATCTNACAAT CAACAGCAAG ATGAAGCTAG GCNTGGGCTT	360
TCGGTAAAAA TAGACTGTGT CTGTCGAAT CAAATGATCT GACCTATCCT CGGTGGCAAG	420
AACTCTTCGA ACCGCTTCCT CAAAGGCNGC TGCCACATTT GTGGCNTCTN TTGCACTTGT	480
TTCAAAA	487

## (2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT AAAAGACTGC ATTTTANAA CTAGCAACTC TTATTCTTT CCTTTAAAAA	60
TACATAGCAT TAAATCCAA ATCTTATTAA AAGACCTGAC AGCTTGAGAA GGTCACTACT	120
GCATTTATAG GACCTCTGG TGGTTCTGCT GTTACNTTTG AANTCTGACA ATCCTTGANA	180
ATCTTTGCAT GCAGAGGAGG TAAAAGGTAT TGGATTTCA CAGAGGAANA ACACAGCGCA	240
GAAATGAAGG GGCCAGGCTT ACTGAGCTTG TCCACTGGAG GGCTCATGGG TGGGACATGG	300
AAAAGAAGGC AGCCTAGGCC CTGGGGAGCC CA	332

## (2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GGGGAGGGCG	TTACTGTTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTGTTGTTCC	GGCCCCATCC	AACCACGAAG	TTGATTTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTAAAGGAC	ATGGAGCTTG	TCACAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTAA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTTGA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCCAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAATTA	CCTGTTACAA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGCCCAG	ACACTGACAT	CAAACTAAGC	CCACTTAGAC	TCCTCACCAAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA	ATCCAGAGTT	GCCATGGAGA	AAATTCCAGT	GTCAGCATTG	TTGCTCCTTG	60
TGGCCCTCTC	CTACACTCTG	GCCAGAGATA	CCACAGTCAA	ACCTGGAGCC	AAAAAGGACA	120
CAAAGGACTC	TCGACCCAAA	CTGCCCGAGA	CCCTCTCCA			159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC	AGACAAAGGC	AGAGGGAGAGA	GCTCTGTTAG	TTCTGTGTTG	TTGAACTGCC	60
ACTGAATTTC	TTTCCACTTG	GACTATTACA	TGCCANTTGA	GGGACTAATG	AAAAAACGTA	120
TGGGGAGATT	TTANCCAATT	TANGNTNTGTA	AATGGGGAGA	CTGGGGCAGG	CGGGAGAGAT	180
TTGCAGGGTG	NAAATGGGAN	GGCTGGTTTG	TTANATGAAC	AGGGACATAG	GAGGTAGGCA	240
CCAGGATGCT	AAATCA					256

(2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTT	TTTGAGATAA	AGCATTGAGA	GAGCTCTCCT	TAACGTGACA	CAATGGAAGG	60
ACTGGAACAC	ATACCCACAT	CTTGTTCTG	AGGGATAATT	TTCTGTATAAA	GTCTTGCTGT	120
ATATTCAAGC	ACATATGTTA	TATATTATTC	AGTTCCATGT	TTATAGCCTA	GTAAAGGAGA	180
GGGGAGATAC	ATTCNGAAAG	AGGACTGAAA	GAAATACTCA	AGTNGGAAAA	CAGAAAAAGA	240
AAAAAAGGAG	CAAATGAGAA	GCCT				264

(2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT	CCAATGCTGA	ATATTTGGCT	TCATTATTCC	CANATTCTTT	GATTGTCAAA	60
GGATTTAATG	TTGTCTCAGC	TTGGGCACCT	CAGTTAGGAC	CTAAGGATGC	CAGCCGGCAG	120
GTTCATATAT	GCAGCAACAA	TATTCAAGCG	CGACAACAGG	TTATTGAACT	TGCCCGGCCAG	180
TTMAATTTC	TTCCCATTGA	CTTGGGATCC	TTATCATCAG	CCAGAGAGAT	TGAAAATTAA	240
CCCCCTACNAC	TCTTTACTCT	CTGGANAGGG	CCAGTGGTGG	TAGCTATAAG	CTTGGCCACA	300
TTTTTTTTTC	CTTTATTCCT	TTGTCAGA				328

(2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC	AGAGCGACAT	ATCCNAGTGT	AGACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAGGCATTG	CTCACTGAAG	GGATAGAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCCTCAT	TCCAAGAGTT	180
TTCAATATTT	GCATGAACCT	GCTGATAANC	CATGTTAANA	AACAAATATC	TCTCTNACCT	240
TCTCATCGGT						250

(2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAATC	CAATGCTGAA	TATTGGCTT	CATTATTCCC	AGATTCTTG	ATTGTCAAAG	60
GATTTAACGT	TGTCTCAGCT	TGGGCACTTC	AGTTAGGACC	TAAGGATGCC	AGCCGGCAGG	120
TTTATATATG	CAGCAACAAT	ATTCAAGCGC	GACAACAGGT	TATGAACCTT	GCCCGCCAGT	180
TGAATTTCAT	TCCCATTGAC	TTGGGATCCT	TATCATCAGC	CANAGAGATT	GAAAATTTAC	240
CCCTACGACT	CTTTACTCTC	TGGAGAGGGC	CAGTGGTGGT	AGCTATAAGC	TTGGCCACAT	300
TTTTTTTTC	TTTATCCCTT	TGTCAGAGAT	GCGATTATC	CATATGCTAN	AAACCAACAG	360
AGTGACTTTT	ACAAAATTCC	TATAGANATT	GTGAATAAAA	CCTTACCTAT	AGTTGCCATT	420
ACTTGCTCT	CCCTAATATA	CCTC				444

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC	AGAGCGACAT	ATCCAAGTGT	ANACTGAATA	AAACTGAATT	CTCTCCAGTT	60
TAAAGCATTG	CTCACTGAAG	GGATAGAAAGT	GACTGCCAGG	AGGGAAAGTA	AGCCAAGGCT	120
CATTATGCCA	AAGGANATAT	ACATTTCAAT	TCTCCAAACT	TCTTCCTCAT	TCCAAGAGTT	180
TTCAATATT	GCATGAACCT	GCTGATAAGC	CATGTTGAGA	AACAAATATC	TCTCTGACCT	240
TCTCATCGGT	AAGCAGAGGC	TGTAGGCAAC	ATGGACCATA	GCGAANAAAA	AACTTAGTAA	300
TCCAAGCTGT	TTTCTACACT	GTAACCAGGT	TTCCAACCAA	GGTGAAATC	TCCTATACTT	360
GGTGCC						366

## (2) INFORMATION FOR SEQ ID NO:216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC	AGAACTCCAC	TGCANGAGGG	AGGGCCGGGC	CAGGAGAATC	TCCGCTTGT	60
CAAGACAGGG	GCCTAAGGAG	GGTCTCCACA	CTGCTNNTAA	GGGCTNTTNC	ATTTTTTAT	120
TAATAAAAAG	TNAAAAGGC	CTCTTCTCAA	CTTTTTTCCC	TTNGGCTGGA	AAATTTAAA	180
ATCAAAAATT	TCCTNAAGTT	NTCAAGCTAT	CATATATACT	NTATCCTGAA	AAAGCAACAT	240

AATTCTTCCT TCCCTCCTTT

260

## (2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTAN AAATGTTATA ATTTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCCAT ATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATT	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCC	240
ATATCCTTCA TGCTTGTAAA GT	262

## (2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCAA CCCCTGAGCA	60
CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTC TTANGTNNA NGTCAGGGT TGCTAGGAAA	180
ANAAATCAGC AGACACAGGT GTAAA	205

## (2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA	114

## (2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGC A GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGA TTCCATGAGG	60
TCTTTGCC C AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC	60
GTTCTTCACC TGTCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAAA	120
ATGTTTGCTG AATTAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA	180
TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT	300
CTCGTATCAA AACAAAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T	351

(2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA	AACAAAAAAA	ACAATTCTTC	ATTCAGAAAA	ATTATCTTAG	GGACTGATAT	60
TGGTAATTAT	GGTCAATTAA	ATWRTRTTK	GGGGCATTTC	CTTACATTGT	CTTGACAAGA	120
TTAAAATGTC	TGTGCCAAAA	TTTTGTATTT	TATTTGGAGA	CTTCTTATCA	AAAGTAATGC	180
TGCCAAAGGA	AGTCTAAGGA	ATTAGTAGTG	TTCCCMTCAC	TTGTTGGAG	TGTGCTATT	240
TAAAAGATTT	TGATTTCCCTG	GAATGACAAT	TATATTTAA	CTTTGGTGGG	GGAAANAGTT	300
ATAGGACCAC	AGTCTTCACT	TCTGATACTT	GTAAATTAAAT	CTTTTATTGC	ACTTGTGTTG	360
ACCATTAAGC	TATATGTTTA	AAA				383

## (2) INFORMATION FOR SEQ ID NO:224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCCTGAAGG	CTTCTTGT	AAAATAGTA	CAGTTACAAC	CAATAGGAAC	AACAAAAAGA	60
AAAAGTTGT	GACATTGTAG	TAGGGAGTGT	GTACCCCTTA	CTCCCCATCA	AAAAAAAAAT	120
GGATACATGG	TTAAAGGATA	RAAGGGCAAT	ATTTTATCAT	ATGTTCTAAA	AGAGAAGGAA	180
GAGAAAATAC	TACITTCCTCR	AAATGGAAGC	CCTTAAAGGT	GCTTGATAAC	TGAAGGACAC	240
AAATGTGGCC	GTCCCATCCTC	CTTARAGTT	GCATGACTTG	GACACGGTAA	CTGTTGCAGT	300
TTTARACTCM	GCATTGTGAC					320

## CLAIMS

1. A method for detecting prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent which is capable of binding to a polypeptide, the polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting prostate cancer in the patient.

2. The method of claim 1 wherein the binding agent is a monoclonal antibody.

3. The method of claim 2 wherein the binding agent is a polyclonal antibody.

4. A method for monitoring the progression of prostate cancer in a patient, comprising:

(a) contacting a biological sample obtained from the patient with a binding agent that is capable of binding to a polypeptide, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences;

(b) determining in the sample an amount of a protein or polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b); and

(d) comparing the amount of polypeptide detected in steps (b) and (c) to monitor the progression of prostate cancer in the patient.

5. A monoclonal antibody that binds to a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 8-29, 41-45, 47-52, 54-65, 70, 73, 74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

6. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient a therapeutically effective amount of a monoclonal antibody according to claim 5.

7. The method of claim 6 wherein the monoclonal antibody is conjugated to a therapeutic agent.

8. A method for detecting prostate cancer in a patient comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotides is specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences; and

(c) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting prostate cancer.

9. The method of claim 8, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

10. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies of claim 5; and
- (b) a detection reagent.

11. A diagnostic kit comprising:

(a) one or more monoclonal antibodies that bind to a polypeptide encoded by a DNA molecule having a nucleotide sequence selected from the group consisting of SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said sequences and variants of said nucleotide sequences; and

- (b) a detection reagent.

12. The kit of claims 10 or 11 wherein the monoclonal antibodies are immobilized on a solid support.

13. The kit of claim 12 wherein the solid support comprises nitrocellulose, latex or a plastic material.

14. The kit of claims 10 or 11 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

15. The kit of claim 14 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

16. The kit of claim 14 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

17. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

18. A diagnostic kit of claim 17 wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

19. A method for detecting prostate cancer in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences and variants of said nucleotide sequences; and
- (c) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting prostate cancer in the patient.

20. The method of claim 19 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

21. A diagnostic kit comprising an oligonucleotide probe specific for a DNA molecule encoding a polypeptide comprising an immunogenic portion of a prostate

protein or a variant thereof, said protein comprising an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224, the complements of said nucleotide sequences variants of said nucleotide sequences.

22. The diagnostic kit of claim 21, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule having a sequence selected from the group consisting of SEQ ID Nos: 2-3, 5-107, 109-111, 115-171, 173-175, 177 and 179-224.

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